



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165030

TO: Louis V Wollenberger
Location: REM-3B61#2C18
Art Unit: 1635
Thursday, September 15, 2005

Case Serial Number: 10/721693

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Wollenberger,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524



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165030

From: Wollenberger, Louis V.
Sent: Wednesday, September 07, 2005 2:32 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request

September 7, 2005

Re: Patent Application No. 10/721,693

CRFE

Please carry out the following sequence searches for the above identified application:

1. A length limited search of oligonucleotide SEQ ID NO:1, where the lower limit is 15 and the upper limit is 30.
2. A length limited search of oligonucleotide SEQ ID NO:2, where the lower limit is 15 and the upper limit is 30.

Thanks,
Louis Wollenberger
Examiner, Art Unit 1635
REM-3B-61, Mailbox 2C-18
x2-8144

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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RESULT 2

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US-10-721-693-4
; Sequence 4, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-4

Query Match      100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
Db 1 AATTCGTTGCTCCGCTCTTGG 21

RESULT 3
US-10-852-997-2
; Sequence 2, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-2

Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
Db 1 AATTCGTTGCTCCGCTCTTGG 21

RESULT 4
US-10-852-997-4
; Sequence 4, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
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; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-4

Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
Db 1 AATTCGTTGCTCCGCTCTTGG 21

RESULT 5
US-10-721-693-1/c
; Sequence 1, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-1

Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCGTTGCTCCGCTCTTGG 21
Db 21 TTCGTTGCTCCGCTCTTGG 3

RESULT 6
US-10-721-693-3/c
; Sequence 3, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-3

Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCGTTGCTCCGCTCTTGG 21
Db 21 TTCGTTGCTCCGCTCTTGG 3
```

```

Db      21  TTGCTGCTCCGCTCTGG 3
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RESULT 7
US-10-852-997-1/c
; Sequence 1, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-1

Query Match      90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  TTGCTGCTCCGCTCTGG 21
      |||||||
Db      21  TTGCTGCTCCGCTCTGG 3
      |||||||

RESULT 8
US-10-852-997-3/c
; Sequence 3, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-3

Query Match      90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  TTGCTGCTCCGCTCTGG 21
      |||||||
Db      21  TTGCTGCTCCGCTCTGG 3
      |||||||

RESULT 9
US-10-719-900-569157
; Sequence 569157, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 569157
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-569157

Query Match      61.9%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AATTCGTTGCTCC 13
      |||||||
Db      5  AATTCGTTGCTCC 17
      |||||||

RESULT 10
US-10-719-900-49468/c
; Sequence 49468, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-49468

Query Match      57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7  TTGCTCCGCTCT 18
      |||||||
Db      21  TTGCTCCGCTCT 10
      |||||||

RESULT 11
US-10-719-900-272193
; Sequence 272193, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 272193
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-272193

```

Query Match 57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGCTCCGCTCTT 19
| | | | | | | |
Db 4 TGCTCCGCTCTT 15

RESULT 12
US-10-719-900-399511/c
; Sequence 399511, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 399511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-399511

Query Match 57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTCGGCTCTTGG 21
| | | | | | | |
Db 23 CTCGGCTCTTGG 12

RESULT 13
US-10-719-900-911843
; Sequence 911843, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 911843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-911843

Query Match 57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCCGCTCT 18
| | | | | | | |
Db 14 TTGCTCCGCTCT 25

RESULT 14
US-10-719-900-911844
; Sequence 911844, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 911844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-911844

Query Match 57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCCGCTCT 18
| | | | | | | |
Db 14 TTGCTCCGCTCT 25

RESULT 15
US-10-719-900-950357/c
; Sequence 950357, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 950357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-950357

Query Match 57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGCTCCGCTCTT 19
| | | | | | | |
Db 24 TGCTCCGCTCTT 13

Search completed: September 12, 2005, 18:20:28
Job time : 279.5 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	10	47.6	25	9	CG712540	CG712540 1119027E0
C 2	10	47.6	28	7	R60473	R60473_yh13g06.r1
C 3	9	42.9	19	8	AZ599480	AZ599480 1M0414C20
C 4	9	42.9	20	8	AJ593450	AJ593450 Arabidops
C 5	9	42.9	22	8	BH905710	BH905710 SALK 1076
C 6	9	42.9	24	9	AJ597633	AJ597633 Arabidops
C 7	9	42.9	25	4	BM399181	BM399181 5009-0-54
C 8	9	42.9	25	4	BM399181	BM399181 5009-0-54
C 9	9	42.9	30	8	AZ861916	AZ861916 2M0168K17
C 10	9	42.9	30	8	BH906585	BH906585 SALK 0339
C 11	8	38.1	30	8	BZ765015	BZ765015 SALK 1278
C 12	8	38.1	18	4	BM398577	BM398577 5009-0-47
C 13	8	38.1	19	7	CF299279	CF299279 7LEAF--03
C 14	8	38.1	20	4	BM397580	BM397580 5009-0-34
C 15	8	38.1	20	4	BM398685	BM398685 5009-0-48
C 16	8	38.1	20	4	BM398964	BM398964 5009-0-51
C 17	8	38.1	20	8	BM398968	BM398968 5009-0-51
C 18	8	38.1	20	8	AZ637794	AZ637794 1M0497D20
C 19	8	38.1	21	4	AZ992248	AZ992248 2M0276N17
C 20	8	38.1	21	4	BM397402	BM397402 5009-0-32
C 21	8	38.1	21	4	BM398984	BM398984 5009-0-51
C 22	8	38.1	21	7	CF333123	CF333123 JMT--01-O
C 23	8	38.1	21	8	AZ636817	AZ636817 1M0495C20
C 24	8	38.1	21	9	AG190199	AG190199 Pan trogl
C 25	8	38.1	22	1	AI723177	AI723177 fc33f01.x

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 47.6%; Score 10; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCTCCGCTCT 18
 |||||
 Db 20 GCTCCGCTCT 11

RESULT 2

R60473 28 bp mRNA linear EST 24-MAY-1995
 LOCUS Yh13g06.r1 Soares infant brain INTB Homo sapiens cDNA clone
 DEFINITION IMAGE:43057 5' similar to SP:SYNP_RAT P22831 ; mRNA sequence.
 ACCESSION R60473 GI:831168
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 28)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

The WashU-Merck EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: M13RP1

High quality sequence stop: 1.

FEATURES

source

1. .28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:415598"
 /db_xref="taxon:9606"
 /clone="IMAGE:43057"
 /sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares infant brain INTB"

/notes="Organ: whole brain; Vector: Lnfmid BA; Site:1: Not

I; Site 2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(dT) primer 15'

AACTGAGAATTCCGGCCGAGGAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lnfmid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 47.6%; Score 10; DB 7; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 TTGCTCCGCT 16
 |||||
 Db 15 TTGCTCCGCT 24

RESULT 3

AZ599480/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0414C20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0414 row: C column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0414C20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCTCGCTC 17
|||||

Db 16 GCTCGCTC 8

RESULT 4
AJ593450
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
380F06, genomic survey sequence.

ACCESSION
AJ593450
VERSION
GSS; left border; T-DNA flanking sequence.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
ORGANISM
Arabidopsis thaliana

REFERENCE
AUTHORS
Brunaud V., Balzergue S., Dubreucq B., Aubourg S., Samson F.,
Chauvin S., Bechtold N., Cruaud C., DeRose R., Pelletier G.,
Lepiniec L., Caboche M. and Lecharny A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
22363535
12445656

REFERENCE
AUTHORS
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

FEATURES
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Massillewskija"
/db_xref="taxon:3702"
/clone="380F06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..20
/notes="T-DNA flanking sequence
left border"

ORIGIN
Query Match 42.9%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCTGCTC 12
|||||

Db 2 TCGTGTCTC 10

RESULT 5
BH905710
LOCUS
DEFINITION
SALK_107640.42.05.x Arabidopsis thaliana T-DNA insertion lines
Arabidopsis thaliana genomic clone SALK_107640.42.05.x, genomic
survey sequence.

ACCESSION
BH905710
VERSION
GSS.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
ORGANISM
Arabidopsis thaliana

REFERENCE
AUTHORS
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R.,
Gadrinab C., Jeske A., Karnes M., Kim C.J., Parker H., Prednis L.,
Shinn P., Zimmerman J. and Ecker J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
T-DNA. This sequence lies within 300 bases of the 5' end of
At3g33595.
Class: TDNA tagged.
Location/Qualifiers
1..22
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/clone="SALK_107640.42.05.x"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 42.9%; Score 9; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCGTTG 9
|||||

Db 10 AATTCGTTG 18
|||||

RESULT 6
AJ597633
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
454D02, genomic survey sequence.

ACCESSION
AJ597633
VERSION
GSS; left border; T-DNA flanking sequence.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
ORGANISM
Arabidopsis thaliana

REFERENCE
AUTHORS
Brunaud V., Balzergue S., Dubreucq B., Aubourg S., Samson F.,
Chauvin S., Bechtold N., Cruaud C., DeRose R., Pelletier G.,
Lepiniec L., Caboche M. and Lecharny A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
22363535
12445656

```

REFERENCE
AUTHORS      2 (bases 1 to 24)
TITLE        Direct Submission
JOURNAL      Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT      Gaston Cremieux, 91057 Evry cedex, FRANCE
              PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).

FEATURES
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            /db_xref="taxon:3702"
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            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    misc_feature
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            /note="T-DNA flanking sequence
            left border"

ORIGIN
Query Match      42.9%; Score 9; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATTCGTTG 9
        |||||
Db      16 AATTCGTTG 24

RESULT 7
BM399181/c
LOCUS      5009-0-54-F03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION      Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399181
VERSION        BM399181.1 GI:18199234
SOURCE        EST.
ORGANISM      Tetrahymena thermophila
              Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
              Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
              Frankel, J. and Klobutcher, L.
TITLE        EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
              Molecular Genetics and Cell Biology
              University of Chicago
              920 E. 58th Street, Chicago, IL 60637, USA
              Tel: 773 702 4374
              Fax: 773 702 3172
              Email: apturkew@midway.uchicago.edu
              Seq primer: T3.
              Location/Qualifiers
                  1..25
                      /organism="Tetrahymena thermophila"
                      /mol_type="mRNA"
                      /strain="CU428.1"
                      /db_xref="taxon:5911"
                      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                      /notes="Vector: Bluescript2 SK+; Details on library
                      preparation can be found in Chilcoat and Turkewitz (2001)
                      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
    source
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            /organism="Tetrahymena thermophila"
            /mol_type="mRNA"
            /strain="CU428.1"
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /notes="Vector: Bluescript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      42.9%; Score 9; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCTCCGCTC 17
        |||||
Db      9 GCTCCGCTC 1

RESULT 8
AZ861916/c
LOCUS      2M0168K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC2M0168K17 R, genomic survey sequence.
ACCESSION      AZ861916
VERSION        AZ861916.1 GI:13058714
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 30)
              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
              Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
              Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
              Niederhausern, A. and Wright, D., Weiss, R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: rdunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0168 row: K column: 17
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 30.
              Location/Qualifiers
                  1..30
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0168K17"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /notes="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high molar excess. The
                      adapted DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of PWD42 (G14732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adapted mouse DNA was annealed to
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

```

ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTCCGCTC 17
|||||
Db 17 GCTCCGCTC 9

RESULT 9

BH906565/c

LOCUS

DEFINITION SALK_033965.21.05.x Arabidopsis thaliana DNA linear GSS 04-SEP-2002
Arabidopsis thaliana genomic clone SALK_033965.21.05.x, genomic survey sequence.

ACCESSION

BH906565

VERSION

BH906565.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 30)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .30

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_033965.21.05.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTG 9
|||||
Db 28 AATTCGTTG 20

RESULT 10

BZ765015/c

LOCUS

DEFINITION SALK_127827.19.55.x Arabidopsis thaliana DNA linear GSS 13-MAR-2003
Arabidopsis thaliana genomic clone SALK_127827.19.55.x, genomic survey sequence.

ACCESSION

BZ765015

VERSION

BZ765015.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 30)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .30

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

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/clone="SALK_127827.19.55.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 42.9%; Score 9; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTG 9
|||||
Db 30 AATTCGTTG 22

RESULT 11

BM398577/c

LOCUS

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
5009-0-47-C10.t.1 Chilcoat/Turkewitz CDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

BM398577

ACCESSION

BM398577.1

VERSION

GI:18198630

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

1 (bases 1 to 18)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

```

Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
    source
        1..18
            Location/Qualifiers
                /organism="Tetrahymena thermophila"
                /mol_type="mRNA"
                /strain="CU428.1"
                /db_xref="taxon:5911"
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                /notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
    Query Match      38.1%; Score 8; DB 4; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1.9e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      9 GCTCCGCT 16
Db      11 GCTCCGCT 4

RESULT 12
CF299279/c
LOCUS
DEFINITION
    7LEAF--03-D20.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-D20, mRNA sequence.
ACCESSION
    CF299279
VERSION
    CF299279.1 GI:33671040
KEYWORDS
    EST.
SOURCE
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
    1 (bases 1 to 19)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
    source
        1..19
            Location/Qualifiers
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
ORIGIN
    Query Match      38.1%; Score 8; DB 7; Length 19;
    Best Local Similarity 100.0%; Pred. No. 1.9e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AATTCGTT 8
Db      12 AATTCGTT 5

Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
    source
        1..18
            Location/Qualifiers
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                /notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
    Query Match      38.1%; Score 8; DB 4; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1.9e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      9 GCTCCGCT 16
Db      11 GCTCCGCT 4

RESULT 13
BM397580/c
LOCUS
DEFINITION
    5009-0-34-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
    BM397580
VERSION
    BM397580.1 GI:18197633
KEYWORDS
    EST.
SOURCE
    Tetrahymena thermophila
    Tetrahymena thermophila
    Tetrahymena thermophila
    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE
    1 (bases 1 to 20)
    Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
    EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
    Contact: Turkewitz AP
    Molecular Genetics and Cell Biology
    University of Chicago
    920 E. 58th Street, Chicago, IL 60637, USA
    Tel: 773 702 4374
    Fax: 773 702 3172
    Email: apturkew@midway.uchicago.edu
    Seq primer: T3.
    Location/Qualifiers
        1..20
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            /mol_type="mRNA"
            /strain="CU428.1"
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ORIGIN
    Query Match      38.1%; Score 8; DB 4; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.9e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      9 GCTCCGCT 16
Db      9 GCTCCGCT 2

RESULT 14
BM398685/c
LOCUS
DEFINITION
    5009-0-48-G09.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
    BM398685
VERSION
    BM398685.1 GI:18198738
KEYWORDS
    EST.
SOURCE
    Tetrahymena thermophila
    Tetrahymena thermophila
    Tetrahymena thermophila
    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE
    1 (bases 1 to 20)
    Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
    EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
    Contact: Turkewitz AP
    Molecular Genetics and Cell Biology
    University of Chicago
    920 E. 58th Street, Chicago, IL 60637, USA
    Tel: 773 702 4374
    Fax: 773 702 3172
    Email: apturkew@midway.uchicago.edu
    Seq primer: T3.
    Location/Qualifiers
        1..20
            /organism="Tetrahymena thermophila"
            /mol_type="mRNA"
            /strain="CU428.1"
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
    Query Match      38.1%; Score 8; DB 4; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.9e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      9 GCTCCGCT 16
Db      9 GCTCCGCT 2

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/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCTCCGCT 16
      |||||
Db      10 GCTCCGCT 3

RESULT 15
BM398964/c
LOCUS      BM398964      20 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM398964
VERSION      BM398964.1 GI:18199017
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 20)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1. .20
Location/Qualifiers
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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QY      9 GCTCCGCT 16
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Search completed: September 12, 2005, 18:09:00
Job time : 1379.5 secs
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 14:13:38 ; Search time 532.5 Seconds
(without alignments)
1910.910 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aaccaagagcggagcaacgaa 21

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1308090

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

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8: gb_pl.*

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13: gb_un.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	6	CQ824576
3	19	90.5	21	6	CQ824575
4	19	90.5	21	6	CQ824577
5	11	52.4	20	6	E30575
6	11	52.4	20	6	AR268863
7	11	52.4	20	6	AR442594
8	11	52.4	22	6	AR568156
9	11	52.4	25	6	AX469952
10	11	52.4	29	6	AR053175
11	11	52.4	30	6	AR098219
12	11	52.4	30	6	BD195066
13	10	47.6	16	6	AR328457
14	10	47.6	17	6	AR243693
15	10	47.6	17	6	AR327452
16	10	47.6	17	6	AR327453
17	10	47.6	17	6	AX736243
18	10	47.6	18	6	AX229718
19	10	47.6	18	6	AX402871

C 20	10	47.6	18	6	AX497756	AX497756 Sequence
C 21	10	47.6	18	6	AX822220	AX822220 Sequence
C 22	10	47.6	18	6	AX825860	AX825860 Sequence
C 23	10	47.6	19	6	AR233719	AR233719 Sequence
C 24	10	47.6	20	6	A51886	A51886 Sequence 50
C 25	10	47.6	20	6	A52459	A52459 Sequence 3
C 26	10	47.6	20	6	AR7520	AR7520 Sequence 1
C 27	10	47.6	20	6	AR085851	AR085851 Sequence
C 28	10	47.6	20	6	AR111715	AR111715 Sequence
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C 30	10	47.6	20	6	AR299168	AR299168 Sequence
C 31	10	47.6	20	6	AR314772	AR314772 Sequence
C 32	10	47.6	20	6	AR314991	AR314991 Sequence
C 33	10	47.6	20	6	AR315108	AR315108 Sequence
C 34	10	47.6	20	6	AR315109	AR315109 Sequence
C 35	10	47.6	20	6	AR337038	AR337038 Sequence
C 36	10	47.6	20	6	AX296790	AX296790 Sequence
C 37	10	47.6	20	6	AX298426	AX298426 Sequence
C 38	10	47.6	20	6	AX743209	AX743209 Sequence
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C 42	10	47.6	21	6	CQ786389	CQ786389 Sequence
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C 45	10	47.6	22	6	AR153363	AR153363 Sequence

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DEFINITION	CQ824574					
ACCESSION	CQ824574					
VERSION	CQ824574.1	GI:49021592				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Kaemmerer, W.F.				
AUTHORS		Treatment of neurodegenerative disease through intracranial				
TITLE		delivery of sirna				
JOURNAL		Patent: WO 2004047872-A 1 10-JUN-2004;				
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VERSION	CQ824576.1	GI:49021596				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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AUTHORS
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Medtronic, Inc. (US)
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 2004047872-A 2 10-JUN-2004;
Medtronic, Inc. (US)
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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AUTHORS
TITLE
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Patent: WO 2004047872-A 4 10-JUN-2004;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Neurogenesis-inductive gene.
E30575
E30575.1 GI:13017145
JP 199341985-A/28.
unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Katsuhiko, M., Jun, A., Kenji, N. and Katsunori, N.
TITLE
Neurogenesis-inductive gene
JOURNAL
Patent: JP 199341985-A 28 14-DEC-1999;
RIKAGAKU KENKYUSHO
OS
Unidentified
PN JP 199341985-A/28
PD 14-DEC-1999
PF 30-APR-1998 JP 1998121456
PR KATSUHIKO MIKOSHIBA, JUN ARIGA, KENJI NAGAI, KATSUNORI MAKATA PC
C12N15/09, A61K35/74, A61K38/76, A61K38/00, A61K48/00, PC
C07K14/47,
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VERSION
Sequence 31 from patent US 650637.
AR268863
AR268863.1 GI:29699559

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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E30575
E30575.1 GI:13017145
JP 199341985-A/28.
unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Katsuhiko, M., Jun, A., Kenji, N. and Katsunori, N.
TITLE
Neurogenesis-inductive gene
JOURNAL
Patent: JP 199341985-A 28 14-DEC-1999;
RIKAGAKU KENKYUSHO
OS
Unidentified
PN JP 199341985-A/28
PD 14-DEC-1999
PF 30-APR-1998 JP 1998121456
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PC A61K37/02, A61K37/02, C12N5/00, (C12N15/00, C12R1/91), (C12N5/00,
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DEFINITION
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VERSION
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AR268863
AR268863.1 GI:29699559

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SOURCE        Unknown.
ORGANISM      Unclassified.
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AUTHORS       Mikoshiba,K., Aruga,J., Nagai,T. and Nakata,K.
TITLE        Neurogenesis inducing genes
JOURNAL      Patent: US 650637-A 31 31-DEC-2002;
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ACCESSION  AR442594
VERSION     AR442594.1 GI:42669851
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Kim,C.M., Park,H.K. and Jang,H.J.
TITLE       Oligonucleotide for detection and identification of Mycobacteria
JOURNAL     Patent: US 6670130-A 202 30-DEC-2003;
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LOCUS      AR568156
DEFINITION Sequence 81 from patent US 6781028.
ACCESSION  AR568156
VERSION     AR568156.1 GI:53986443
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Costa,M.R., Doberstein,S.K., Elson,S.L., Ferguson,K.C. and
             Homburger,S.A.
TITLE       Animal models and methods for analysis of lipid metabolism and
             screening of pharmaceutical and pesticidal agents that modulate
             lipid metabolism
JOURNAL     Patent: US 6781028-A 81 24-AUG-2004;
FEATURES    Location/Qualifiers
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AUTHORS       Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE        Gene sequence for spinocerebellar ataxia type 1 and method for
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JOURNAL      Patent: US 5834183-A 81 10-NOV-1998;
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LOCUS      AX469952
DEFINITION Sequence 69 from Patent WO2053771.
ACCESSION  AX469952
VERSION     AX469952.1 GI:22205225
KEYWORDS
SOURCE      Escherichia coli
ORGANISM    Escherichia coli
REFERENCE   1
AUTHORS     Berghof,K., Grabowski,R., Groenewald,C. and Pardigol,A.
TITLE       Detection of pathogenic bacteria
JOURNAL     Patent: WO 02053771-A 69 11-JUL-2002;
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Db      23 ACCAGAGCGG 13

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ACCESSION  AR053175
VERSION     AR053175.1 GI:5978037
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE       Gene sequence for spinocerebellar ataxia type 1 and method for
             diagnosis
JOURNAL      Patent: US 5834183-A 81 10-NOV-1998;
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DEFINITION    Sequence 42 from patent US 6074851.
ACCESSION     AR098219
VERSION       AR098219.1  GI:12807476
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 30)
AUTHORS      Daibei,M.R. Jr., Yem,A.W. and Wolfe,C.L.
TITLE        Catalytic macro molecules having cdc25B like activity
JOURNAL      Patent: US 6074851-A 42 13-JUN-2000;
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DEFINITION    Catalytic polymer having CDC25B like activity.
ACCESSION     BD195066
VERSION       BD195066.1  GI:33004824
KEYWORDS      JP 2002515742-A/27.
SOURCE        unidentified
ORGANISM      unidentified
REFERENCE     1 (bases 1 to 30)
AUTHORS      Jr,M.R.D., Yem,A.W. and Wilson,C.L.
TITLE        Catalytic polymer having CDC25B like activity
JOURNAL      Patent: JP 2002515742-A 27 28-MAY-2002;
COMMENT      PHARMACIA & UPJOHN CO
OS           Unidentified
PN           JP 2002515742-A/27
PD           28-MAY-2002
PF           02-MAY-1997 JP 1997538892
PR           02-MAY-1996 US 60/016748, 07-MAY-1996 US 60/017323 PI
MARTIN R DEIBEL JR,ANTHONY W YEM,CINDY L WILSON PC
(C12N15/55,C12N15/54,C12N15/62,C12N9/16,C12N9/10,C12N1/21// PC
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DEFINITION    Sequence 5859 from patent US 6566127.
ACCESSION     AR328457
VERSION       AR328457.1  GI:33714265
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 16)
AUTHORS      Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6566127-A 5859 20-MAY-2003;
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ACCESSION     AR243693
VERSION       AR243693.1  GI:27291128
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 17)
AUTHORS      Cazaux,C., Tiraby,G.J., Fons,P. and Hoffmann,J.-S.
TITLE        Use of a vector expressing DNA polymerase .beta. as medicine
JOURNAL      Patent: US 6475996-A 5 05-NOV-2002;
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ACCESSION     AR327452
VERSION       AR327452.1  GI:33713260
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions

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related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4854 20-MAY-2003;
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Db 7 ACCAAGAGCG 16

Search completed: September 12, 2005, 17:22:23
Job time : 536.5 secs

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 16:40:43 ; Search time 58 Seconds
(without alignments)
592.445 Million cell updates/sec

Title: US-10-721-693-2

Perfect score: 21

Sequence: 1 aattcggtgctcgctctgg 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 914340

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	57.1	22	4	US-09-332-522E-81
2	11	52.4	20	3	US-09-121-920-26/c
3	11	52.4	20	3	US-09-172-045-31
4	11	52.4	20	4	US-09-342-325C-31
5	11	52.4	20	4	US-09-980-052-202
6	11	52.4	22	5	PCT-US93-12078-2
7	11	52.4	22	5	PCT-US93-12078-3
8	11	52.4	25	4	US-09-396-196G-14051
9	11	52.4	25	4	US-09-396-196G-18109
10	11	52.4	25	4	US-09-396-196G-18110
11	11	52.4	25	4	US-09-396-196G-18111
12	11	52.4	25	4	US-09-396-196G-66426
13	11	52.4	25	4	US-09-396-196G-66427
14	11	52.4	25	4	US-09-396-196G-66438
15	11	52.4	30	3	US-08-848-810-42
16	11	52.4	30	3	US-09-492-985-6
17	10	47.6	18	3	US-09-344-521-22
18	10	47.6	20	3	US-08-875-223-3
19	10	47.6	20	4	US-09-198-452A-5309
20	10	47.6	20	4	US-09-198-452A-5645
21	10	47.6	20	4	US-09-198-452A-5646
22	10	47.6	20	4	US-09-922-146-11
23	10	47.6	20	4	US-10-023-649A-19
24	10	47.6	21	3	US-09-210-896-22
25	10	47.6	22	3	US-08-793-044-7
26	10	47.6	23	3	US-09-102-831-16
27	10	47.6	24	3	US-09-284-900-2

c	28	10	47.6	24	4	US-09-270-767-62514	Sequence 62514, A
c	29	10	47.6	25	1	US-08-379-926A-4	Sequence 4, Appli
c	30	10	47.6	25	3	US-08-866-446-1	Sequence 1, Appli
c	31	10	47.6	25	4	US-09-396-196G-12977	Sequence 12977, A
c	32	10	47.6	25	4	US-09-396-196G-12978	Sequence 12978, A
c	33	10	47.6	25	4	US-09-396-196G-34741	Sequence 34741, A
c	34	10	47.6	25	4	US-09-396-196G-52807	Sequence 52807, A
c	35	10	47.6	25	4	US-09-396-196G-52808	Sequence 52808, A
c	36	10	47.6	25	4	US-09-396-196G-52809	Sequence 52809, A
c	37	10	47.6	25	4	US-09-396-196G-56973	Sequence 56973, A
c	38	10	47.6	25	4	US-09-396-196G-73270	Sequence 73270, A
c	39	10	47.6	25	4	US-09-396-196G-73271	Sequence 73271, A
c	40	10	47.6	25	4	US-09-396-196G-77212	Sequence 77212, A
c	41	10	47.6	25	4	US-09-396-196G-87841	Sequence 87841, A
c	42	10	47.6	25	4	US-09-396-196G-96977	Sequence 96977, A
c	43	10	47.6	25	4	US-09-396-196G-96978	Sequence 96978, A
c	44	10	47.6	25	4	US-09-396-196G-96979	Sequence 96979, A
c	45	10	47.6	25	4	US-09-396-196G-96980	Sequence 96980, A

ALIGNMENTS

RESULT 1
US-09-332-522E-81
; Sequence 81, Application US/09332522E
; Patent No. 6781028
; GENERAL INFORMATION:
; APPLICANT: Costa, M.
; APPLICANT: Doberstein, S.
; APPLICANT: Elson, S.
; APPLICANT: Ferguson, K.
; APPLICANT: Homburger, S.
; TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND S
; TITLE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METAB
; FILE REFERENCE: 7326-101, EX99-004
; CURRENT APPLICATION NUMBER: US/09/332,522E
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 81
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-332-522E-81

Query Match 57.1%; Score 12; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATTCTGTTGCTCC 13
| | | | | | | | | |
Db 11 ATTCTGTTGCTCC 22

RESULT 2
US-09-121-920-26/c
; Sequence 26, Application US/09121920
; Patent No. 6066460
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Mark W.
; APPLICANT: Kinoshita, No. 6066460iyuki
; TITLE OF INVENTION: METHOD FOR CLONING SECRETED PROTEINS
; FILE REFERENCE: HMV-022.01
; CURRENT APPLICATION NUMBER: US/09/121,920
; CURRENT FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 60/053,586
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26

; LENGTH: 20
; TYPE: DNA
; ORGANISM: primer
US-09-121-920-26

Query Match 52.4%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGCTCTTG 20
| | | | | | | | | |
Db 11 CTCGCTCTTG 1

RESULT 3

US-09-172-045-31/c
; Sequence 31, Application US/09172045
; Patent No. 6277594

; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko

; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu

; APPLICANT: Nakata, Katsunori
; TITLE OF INVENTION: Neurogenesis Inducing Gene

; FILE REFERENCE: Hiraki-03497
; CURRENT APPLICATION NUMBER: US/09/172,045

; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: JP98/86979

; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP98/121456

; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31

; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-172-045-31

Query Match 52.4%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGCTCTTG 20
| | | | | | | | | |
Db 11 CTCGCTCTTG 1

RESULT 4

US-09-342-325C-31/c
; Sequence 31, Application US/09342325C
; Patent No. 6500637

; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko

; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu

; APPLICANT: Katsunori, Nakata
; TITLE OF INVENTION: Neurogenesis Inducing Gene

; FILE REFERENCE: HIRAKI-03814
; CURRENT APPLICATION NUMBER: US/09/342,325C

; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: JP98/86979

; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: JP98/121456

; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 09/172,045

; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31

; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-342-325C-31

Query Match 52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGCTCTTG 20
| | | | | | | | | |
Db 11 CTCGCTCTTG 1

RESULT 5

US-09-980-052-202

; Sequence 202, Application US/099800052
; Patent No. 6670130

; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.

; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung

; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT

; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29

; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71

; SEQ ID NO 202
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium porcinum
US-09-980-052-202

Query Match 52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTTGCTCCGCT 16
| | | | | | | | | |
Db 10 GTTGCTCCGCT 20

RESULT 6

PCT-US93-12078-2/c

; Sequence 2, Application PC/TUS9312078
; GENERAL INFORMATION:

; APPLICANT:
; APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS

; APPLICANT: SYSTEM: 201 West 7th Street

; APPLICANT: STREET: Austin

; APPLICANT: CITY: Texas

; APPLICANT: STATE: United States of America

; APPLICANT: COUNTRY: 78701

; APPLICANT: POSTAL CODE: (512)499-4462

; APPLICANT: TELEPHONE NO: (512)499-4523

; APPLICANT: TELEFAX: POTENT AND SPECIFIC

; TITLE OF INVENTION:


```

; TITLE OF INVENTION: CHEMICALLY-CONJUGATED
; NUMBER OF INVENTIONS: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12078
; FILING DATE: UNKNOWN
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/992,900
; FILING DATE: 16.12.92
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTFF046PCT
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2676
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-12078-2

Query Match 52.4%; Score 11; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTCGTTGCTC 12
Db 11 ATTCGTTGCTC 1

RESULT 7
PCT-US93-12078-3
; Sequence 3, Application PC/TUS9312078
; GENERAL INFORMATION:
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF TEXAS
; APPLICANT NAME: SYSTEM
; APPLICANT STREET: 201 West 7th Street
; APPLICANT CITY: Austin
; APPLICANT STATE: Texas
; APPLICANT COUNTRY: United States of America
; APPLICANT POSTAL CODE: 78701
; APPLICANT TELEPHONE NO: (512)499-4462
; APPLICANT TELEFAX: (512)499-4523
; TITLE OF INVENTION: POTENT AND SPECIFIC
; TITLE OF INVENTION: CHEMICALLY-CONJUGATED
; TITLE OF INVENTION: IMMUNOTOXINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12078
; FILING DATE: UNKNOWN
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/992,900
; FILING DATE: 16.12.92
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTFF046PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2676
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US93-12078-3

Query Match 52.4%; Score 11; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTCGTTGCTC 12
Db 12 ATTCGTTGCTC 22

RESULT 8
US-09-396-196G-14051/c
; Sequence 14051, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-14051

Query Match 52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCCGCTCTTGG 21
Db 17 TCCGCTCTTGG 7

RESULT 9
US-09-396-196G-18109
; Sequence 18109, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:

```

```
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18109

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCGCTCTTGG 21
Db      15 TCCGCTCTTGG 25
|||||

RESULT 10
US-09-396-196G-18110
; Sequence 18110, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18110

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCGCTCTTGG 21
Db      15 TCCGCTCTTGG 25
|||||

RESULT 11
US-09-396-196G-18111
; Sequence 18111, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18109

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TCCGCTCTTGG 21
Db      15 TCCGCTCTTGG 25
|||||

RESULT 12
US-09-396-196G-66426/c
; Sequence 66426, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-66426

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TTGCTCCGCTC 17
Db      24 TTGCTCCGCTC 14
|||||

RESULT 13
US-09-396-196G-66427/c
; Sequence 66427, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-66427
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Query Match 52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17
| | | | | | | | | |
Db 22 TTGCTCCGCTC 12

RESULT 14
US-09-396-196G-66438/c
; Sequence 66438, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66438

Query Match 52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17
| | | | | | | | | |
Db 20 TTGCTCCGCTC 10

RESULT 15
US-08-848-810-42/c
; Sequence 42, Application US/08848810
; Patent No. 6074851
; GENERAL INFORMATION:
; APPLICANT: Deibel Jr., M. R.
; APPLICANT: Yem, A. W.
; APPLICANT: Wilson, C. L.
; TITLE OF INVENTION: Catalytic Macro Molecules Having DCD25B
; TITLE OF INVENTION: Like Activity
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn Company
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/848,810
; APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-833-7914

TELEFAX: 616-833-6897
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-848-810-42

Query Match 52.4%; Score 11; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17
| | | | | | | | | |
Db 14 TTGCTCCGCTC 4

Search completed: September 12, 2005, 18:11:00
Job time : 58 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 14:04:18 ; Search time 174 Seconds
(without alignments)
714.452 Million cell updates/sec

Title: US-10-721-693-2

Perfect score: 21

Sequence: 1 aattcgtgtcctcgtcttgg 21

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2557800

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	12 ADP44614	Adp44614 Antlense
2	21	100.0	21	12 ADP44612	Adp44612 Antlense
3	19	90.5	21	12 ADP44613	Adp44613 Sense DNA
4	19	90.5	21	12 ADP44611	Adp44611 Sense DNA
5	12	57.1	20	2 AAZ03368	Aaz03368 PCR prime
6	12	57.1	30	6 AAL48427	Aal48427 Secreted
7	11	52.4	19	12 ADK96972	Adk96972 Primer of
8	11	52.4	20	2 AAX19405	Aax19405 Neurogeni
9	11	52.4	20	2 AAZ04279	Aaz04279 PCR prime
10	11	52.4	20	3 AAZ55953	Aaz55953 Xenopus 1
11	11	52.4	20	4 AAF23328	Aaf23328 Oligonucl
12	11	52.4	20	10 ADD56623	Add56623 Human gen
13	11	52.4	20	10 ABZ97696	Abz97696 Human CCR
14	11	52.4	20	10 ABZ97695	Abz97695 Human CCR
15	11	52.4	20	11 ABD30726	Abd30726 Human CCR
16	11	52.4	20	11 ABD30727	Abd30727 Human CCR
17	11	52.4	20	12 ADJ59552	Adj59552 Oligonucl
18	11	52.4	20	12 ADJ59553	Adj59553 Oligonucl
19	11	52.4	20	12 ADO45043	Ado45043 Human oli
20	11	52.4	20	12 ADO45042	Ado45042 Human oli

C	21	11	52.4	22	2	AAQ68396	Pseudomon
C	22	11	52.4	29	2	AAx80489	Aax80489 Human sec
C	23	11	52.4	29	4	AAS59324	Aas59324 Human sec
C	24	11	52.4	29	6	ABA90993	AbA90993 Biotinyla
C	25	11	52.4	29	12	ADO61037	Ado61037 Human deb
C	26	11	52.4	30	2	AAQ78253	Aaq78253 Primer to
C	27	11	52.4	30	3	AAa50463	Aaa50463 Human zin
C	28	10	47.6	17	2	AAV96406	Aav96406 Potato ci
C	29	10	47.6	17	2	AAV96405	Aav96405 Potato ci
C	30	10	47.6	17	6	ACN01300	Acn01300 WNV Hamme
C	31	10	47.6	17	6	ACN12384	Acn12384 WNV minus
C	32	10	47.6	17	6	ACN14271	Acn14271 WNV minus
C	33	10	47.6	17	6	ACN04597	Acn04597 WNV Zinzy
C	34	10	47.6	17	6	ACN14270	Acn14270 WNV minus
C	35	10	47.6	17	6	ACN03280	Acn03280 WNV Inozy
C	36	10	47.6	17	6	ACN04596	Acn04596 WNV Zinzy
C	37	10	47.6	17	6	ACN12383	Acn12383 WNV minus
C	38	10	47.6	17	6	ACN01301	Acn01301 WNV Hamme
C	39	10	47.6	17	6	ACN03279	Acn03279 WNV Inozy
C	40	10	47.6	17	6	ACN09757	Acn09757 WNV minus
C	41	10	47.6	17	10	ADI49330	Adi49330 Human tum
C	42	10	47.6	18	3	AAa52028	Aaa52028 Antisense
C	43	10	47.6	18	5	AAa52190	Aaa52190 Human Int
C	44	10	47.6	18	6	AAa40983	Aaa40983 Human PI3
C	45	10	47.6	18	6	ABK29394	Abk29394 Penicilli

ALIGNMENTS

RESULT 1
ADP44614
ID ADP44614 standard; DNA; 21 BP.

AC ADP44614;

XX 26-AUG-2004 (first entry)

DE Antlense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.

XX neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;

KW Huntington's; spinocerebellar ataxia type 1;

KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;

KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;

KW small interfering RNA; ss; human; ataxin 1.

XX Homo sapiens.

XX WO2004047872-A2.

PD 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US037650.

XX 26-NOV-2002; 2002US-0429387P.

PR 03-FEB-2003; 2003US-0444614P.

XX (MEDT) MEDTRONIC INC.

XX Kaemmerer WF;

XX WPI; 2004-441106/41.

PT New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.

XX Claim 68; SEQ ID NO 4; 228pp; English.

XX The invention relates to a novel medical system for treating a

CC neurodegenerative disorder comprising an intracranial access device, a

CC mapping means for locating a predetermined location in the brain, a

CC deliverable amount of a small interfering RNA (siRNA), or vector encoding

CC the siRNA, and a delivery means. The system of the invention has
CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the antisense DNA 2 encoding an siRNA
CC targeted to human ataxin 1 mRNA of the invention.
XX SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
|||||
Db 1 AATTCGTTGCTCCGCTCTTGG 21
|||||

RESULT 2
ADP44612
ID ADP44612 standard; DNA; 21 BP.
XX
AC ADP44612;
XX
DT 26-AUG-2004 (first entry)
XX
DE Antisense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
XX
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
KW Huntington's; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
KW small interfering RNA; ss; human; ataxin 1.
XX
OS Homo sapiens.
XX
PN WO2004047872-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037650.
XX
PR 26-NOV-2002; 2002US-0429387P.
PR 03-FEB-2003; 2003US-0444614P.
XX
PA (MEDT) MEDTRONIC INC.
XX
PI Kaemmerer WF;
XX
DR WPI; 2004-441106/41.
XX
PT New medical system comprising an intracranial access device, a mapping
PT means, a small interfering RNA or vector encoding the RNA, and a delivery
PT means, useful for treating a neurodegenerative disorder.
XX
PS Claim 68; SEQ ID NO 2; 228pp; English.
XX
CC The invention relates to a novel medical system for treating a
CC neurodegenerative disorder comprising an intracranial access device, a
CC mapping means for locating a predetermined location in the brain, a
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
CC the siRNA, and a delivery means. The system of the invention has
CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the antisense DNA 1 encoding an siRNA
CC targeted to human ataxin 1 mRNA of the invention.
XX SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCTCCGCTCTTGG 21
|||||
Db 1 AATTCGTTGCTCCGCTCTTGG 21
|||||

RESULT 3
ADP44613/c
ID ADP44613 standard; DNA; 21 BP.
XX
AC ADP44613;
XX
DT 26-AUG-2004 (first entry)
XX
DE Sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.
XX
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
KW Huntington's; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
KW small interfering RNA; ss; human; ataxin 1.
XX
OS Homo sapiens.
XX
PN WO2004047872-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037650.
XX
PR 26-NOV-2002; 2002US-0429387P.
PR 03-FEB-2003; 2003US-0444614P.
XX
PA (MEDT) MEDTRONIC INC.
XX
PI Kaemmerer WF;
XX
DR WPI; 2004-441106/41.
XX
PT New medical system comprising an intracranial access device, a mapping
PT means, a small interfering RNA or vector encoding the RNA, and a delivery
PT means, useful for treating a neurodegenerative disorder.
XX
PS Claim 68; SEQ ID NO 3; 228pp; English.
XX
CC The invention relates to a novel medical system for treating a
CC neurodegenerative disorder comprising an intracranial access device, a
CC mapping means for locating a predetermined location in the brain, a
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
CC the siRNA, and a delivery means. The system of the invention has
CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the sense DNA 2 encoding an siRNA
CC targeted to human ataxin 1 mRNA of the invention.
XX SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCGTTGCTCCGCTCTTGG 21
|||||
Db 21 TTCGTTGCTCCGCTCTTGG 3
|||||

RESULT 4
ADP44611/c
ID ADP44611 standard; DNA; 21 BP.

XX ADP44611;
 AC 26-AUG-2004 (first entry)
 DT Sense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
 DE neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
 KW Huntington's; spinocerebellar ataxia type 1;
 KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
 KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
 KW small interfering RNA; ss; human; ataxin 1.
 XX Homo sapiens.
 OS
 XX WO2004047872-A2.
 PN 10-JUN-2004.
 PD 26-NOV-2003; 2003WO-US037650.
 XX 26-NOV-2002; 2002US-0429387P.
 PR 03-FEB-2003; 2003US-0444614P.
 XX (MEDT) MEDTRONIC INC.
 PA Kaemmerer WF;
 XX WPI; 2004-441106/41.
 DR New medical system comprising an intracranial access device, a mapping
 XX means, a small interfering RNA or vector encoding the RNA, and a delivery
 PT means, useful for treating a neurodegenerative disorder.
 PT Claim 68; SEQ ID NO 1; 228pp; English.
 PS The invention relates to a novel medical system for treating a
 CC neurodegenerative disorder comprising an intracranial access device, a
 CC mapping means for locating a predetermined location in the brain, a
 CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
 CC the siRNA, and a delivery means. The system of the invention has
 CC applications related to the CNS and may be useful for treating a
 CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
 CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
 CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
 CC The current sequence is that of the sense DNA 1 encoding an siRNA
 CC targeted to human ataxin 1 mRNA of the invention.
 XX Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 SQ Query Match 90.5%; Score 19; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTGCTTCTCCGCTCTTGG 21
 |||||
 DB 21 TTGCTTCTCCGCTCTTGG 3
 RESULT 5
 AAZ03368/c
 ID AAZ03368 standard; DNA; 20 BP.
 XX AC AAZ03368;
 AC 07-OCT-1999 (first entry)
 DT PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihemphatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX Synthetic.
 OS Chlamydia trachomatis.
 XX WO9928475-A2.
 PN 10-JUN-1999.
 PD 27-NOV-1998; 98WO-IB001939.
 XX 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.
 XX (GEST) GENSET.
 XX Griffais R;
 XX WPI; 1999-371125/31.
 DR Genome sequence of Chlamydia trachomatis.
 XX Disclosure; Page 1601; 1755pp; English.
 CC PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,
 CC epididymitis, cervicitis, salpingitis, perihemphatitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 XX diseases
 XX Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 SQ Query Match 57.1%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTCGTTGCTCC 13
 |||||
 DB 13 ATTCGTTGCTCC 2
 RESULT 6
 AAL48427
 ID AAL48427 standard; DNA; 30 BP.
 XX AC AAL48427;
 XX 03-OCT-2002 (first entry)
 DT Secreted Chlamydia proteins related construct Inca/myCHIS PCR primer #2.
 XX Chlamydia; secreted protein; type III secretion pathway; Inc; cya;
 KW vaccine; chlamydial infection; antibacterial; antiatherosclerotic; PCR;
 KW primer; ss.
 XX Unidentified.
 OS Synthetic.
 OS WO200248185-A2.
 PN 20-JUN-2002.
 PD 13-DEC-2001; 2001WO-IB002808.
 PF 14-DEC-2000; 2000US-0255118P.
 XX

PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Subtil A, Parsot C, Dautry-Varsat A;
XX WPI; 2002-583484/62.
DR
XX
XX Novel purified secreted Chlamydia polypeptide which is identified by its
PT secretion in a Gram-negative bacterial strain containing a type III
PT secretion pathway, useful for treating Chlamydia infections in humans.
XX
XX Example 1; Page 28; 57pp; English.
XX
XX The present invention relates to a purified secreted Chlamydia protein,
CC which is identified by its expression by a Gram-negative bacterial strain
CC and secretion by the type III secretion pathway of the bacterium. This
CC can be used to diagnose, treat and vaccinate against Chlamydia infection
CC in a patient, which may contribute to atherosclerosis or a sexually
CC transmitted disease. The present sequence is a PCR primer used to produce
CC fusion constructs in the exemplification of the invention
XX
XX Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 U; 0 Other;
SQ

Query Match 57.1%; Score 12; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATTCGTTGCTC 12
| | | | | | | |
DB 6 AATTCGTTGCTC 17

RESULT 7
ADK96972/c
ID ADK96972 standard; DNA; 19 BP.
AC ADK96972;
XX
XX 06-MAY-2004 (first entry)
XX
XX Primer of the invention #2692.
XX
XX human; single nucleotide polymorphism; SNP; ss; primer.
XX
XX Synthetic.
XX
XX JP2003259875-A.
XX
XX 16-SEP-2003.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2004-093977/10.
XX
XX Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 6001; 2627pp; Japanese.
XX
XX The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
XX Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
SQ

Query Match 52.4%; Score 11; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8e+03; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TGCTCGCTCT 18
| | | | | | | |
DB 15 TGCTCGCTCT 5

RESULT 8
AAK19405/c
ID AAK19405 standard; DNA; 20 BP.
XX
XX AAK19405;
XX
XX 19-MAY-1999 (first entry)
XX
XX Neurogenin protein PCR forward primer.
DE
XX Secreted protein; microsome; signal peptide; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO9905256-A2.
PN
XX 04-FEB-1999.
PD
XX
XX 24-JUL-1998; 98WO-US015394.
PF
XX
XX 24-JUL-1997; 97US-0053586P.
PR
XX
XX (HARD) HARVARD COLLEGE.
PA
XX
XX Kirschner MW, Kinoshita N;
PI
XX WPI; 1999-153316/13.
DR
XX
XX Isolating nucleic acids encoding proteins comprising a signal peptide -
PT by translating RNA and isolating translated RNA that is associated with
PT microsomes, useful as therapeutic agents.
XX
XX Example 2; Page 34; 45pp; English.
XX
XX The present invention describes the isolation of nucleic acid (I) that
CC encodes a protein (II) having a signal peptide (SP), which comprises
CC isolating RNA molecules (III) that are associated with microsomes under
CC conditions where (III) is at least partly translated. Also described are:
CC (1) a library of (I) encoding (II) comprising SP; (2) (I) isolated by the
CC above method; and (3) (II) encoded by (I) (I) and (II) are useful
CC therapeutically, typically (II) are cell growth factors such as
CC cytokines, interleukins, colony-forming factors, possibly useful in
CC treatment of cancer. (I) are also used; as tissue and molecular weight
CC markers; as chromosome tags; to detect possible genetic disorders; as
CC hybridisation probes to identify related nucleic acid; as primers for DNA
CC fingerprinting; to generate antibodies; and in interaction trap assays to
CC identify gene encoding specific binding agents. (II) are useful in drug
CC screening, for raising antibodies (e.g. for use as immunoassay reagents)
CC and to induce an immune response. The method is more efficient and
CC reliable than the sequence trap system. It does not involve formation of
CC a fusion protein (rather natural proteins are selected) and (II) do not
CC have to be secreted. The present sequence represents a PCR primer which
CC is used in an example from the present invention
XX
XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
SQ

Query Match 52.4%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTCGCTCTTG 20
| | | | | | | |
DB 11 CTCGCTCTTG 1


```

RESULT 9
AAZ04279/c
ID AAZ04279 standard; DNA; 20 BP.
XX AC
XX AAZ04279;
XX 07-OCT-1999 (first entry)
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
XX Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX OS
XX Synthetic.
XX Chlamydia trachomatis.
XX WO928475-A2.
XX 10-JUN-1999.
XX PD
XX PF 27-NOV-1998; 98WO-18001939.
XX PR 28-NOV-1997; 97FR-00015041.
XX PR 17-DEC-1997; 97FR-00016034.
XX PR 04-NOV-1998; 98US-0107077P.
XX PA (GEST ) GENSET.
XX PI
XX Griffais R;
XX WPI; 1999-371125/31.
XX Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1675; 1755pp; English.
XX PCR primers AAZ01426-206209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
XX conjunctivitis; genital diseases such as nongonococcal urethritis,
XX epididymitis, cervicitis, salpingitis, perihhepatitis, Bartholinitis;
XX pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
XX The polypeptides of the invention may be of use in treating these
XX diseases
XX
XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 52.4%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TCCTTGCTCCG 14
DB 15 TCCTTGCTCCG 5
RESULT 10
AAZ55953/c
ID AAZ55953 standard; cDNA; 20 BP.
XX AC
XX AAZ55953;
XX 10-APR-2000 (first entry)
XX DE
XX Xenopus laevis neurogenin sense PCR primer, SEQ ID NO:31.
XX

```

```

KW Neurogenin; Zic3; zinc finger; neuroregeneration; neurological disease;
KW diagnosis; Alzheimer's disease; expression pattern; PCR primer; ss.
XX Xenopus laevis.
XX OS
XX JPI1341985-A.
XX PD
XX 14-DEC-1999.
XX PF
XX 30-APR-1998; 98JP-00121456.
XX PR
XX 31-MAR-1998; 98JP-00086979.
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX WPI; 2000-101694/09.
XX A nerve formation-inducing gene - useful as a diagnostic agent for
XX nervous diseases, and for treating Alzheimer disease.
XX Example 2; Page 14; 30pp; Japanese.
XX The invention relates to Xenopus laevis Zic3 protein (AAZ69524). Zic3
XX contains a zinc finger motif, and induces the formation of neurons. The
XX cDNA was obtained from embryonic Xenopus nerve poly(A+) RNA. Zic3, and
XX nucleotides encoding it, are useful as diagnostic tools for neurological
XX diseases, and for the treatment of Alzheimer's disease. Sequences
XX AAZ55931-Z55962 represent PCR primers used to determine which other genes
XX are expressed with Zic3 in various Xenopus cell types in an
XX exemplification of the present invention
XX
XX Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 52.4%; Score 11; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 CTCGGCTCTTG 20
DB 11 CTCGGCTCTTG 1
RESULT 11
AAZ23328
ID AAZ23328 standard; DNA; 20 BP.
XX AC
XX AAF23328;
XX 19-MAR-2001 (first entry)
XX DE
XX Oligonucleotide for detection of Mycobacterium porcinum.
XX ITS; internal transcribed spacer region; Mycobacterium fortuitum;
XX Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
XX Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
XX Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
XX Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
XX OS
XX Mycobacterium porcinum.
XX WO200073436-A1.
XX PD
XX 07-DEC-2000.
XX PF
XX 16-MAY-2000; 2000WO-KR000477.
XX PR
XX 29-MAY-1999; 99KR-00019631.
XX PR
XX 29-MAY-1999; 99KR-00019632.
XX PR
XX 29-MAY-1999; 99KR-00019633.
XX PR
XX 29-MAY-1999; 99KR-00019634.
XX PR
XX 29-MAY-1999; 99KR-00019635.
XX PR
XX 07-APR-2000; 2000KR-00018189.
XX

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PA (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
XX Kim CM, Park HK, Jang HJ;
XX WPI; 2001-061527/07.
XX
XX Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
XX Claim 34; Page 78; 89pp; English.
XX
XX The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC diernhoferi genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
XX Sequence 20 BP; 0 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GTTGCTCCGCT 16
DB 10 GTTGCTCCGCT 20
|||||
RESULT 12
ADP56623
ID ADD56623 standard; DNA; 20 BP.
XX
XX ADD56623;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human gene expression analysis multiplex Start-PCR primer #143.
XX
XX Gene expression; multiplex standardised reverse transcriptase-PCR;
XX Start-PCR; high density oligonucleotide array; cDNA array;
XX Small biological sample; fine needle aspirate biopsy;
XX laser captured microdissected material; human; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003186246-A1.
XX
XX 02-OCT-2003.
XX
XX 28-MAR-2002; 2002US-00109349.
XX
XX 28-MAR-2002; 2002US-00109349.
XX
XX (WILL/) WILLEY J C.
XX PA (CRAW/) CRAWFORD E L.
XX
XX Willey JC, Crawford EL;
WPI; 2003-811730/76.
Direct comparison of numerical gene expression values between samples of
genes comprises using multiplex standardized reverse transcription-
polymerase chain reaction.
Example 1; SEQ ID NO 143; 59pp; English.
The present invention relates to a method for the direct comparison of
numerical gene expression values between samples of genes. The method
comprises amplifying cDNA in the presence of a competitive template
mixture and primer pairs for several genes and then amplifying aliquots
of the PCR products using a primer pair specific for each gene. The
method of amplification is by multiplex standardised reverse
transcriptase-polymerase chain reaction (Start-PCR). High density
oligonucleotide or cDNA arrays are used to measure PCR products following
quantitative Start-PCR. The method is useful for the assessment of gene
expression in small biological samples such as fine needle aspirate
biopsies, and laser captured microdissected materials. The method allows
for the standardised measurement of hundreds of genes from the same
sample, which in prior art, could only be assessed for one gene. The
present sequence represents a multiplex Start-PCR primer which can be
used in the method of the present invention.
Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TTTCGTTGCTCC 13
DB 8 TTTCGTTGCTCC 18
|||||
RESULT 13
AB297696
ID AB297696 standard; DNA; 20 BP.
XX
XX AB297696;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human CCR3 oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; lung; adenosine sensitivity;
XX lung inflammation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

```

```

PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12938; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCCGCTC 17
Db 1 TTGCTCCGCTC 11

RESULT 14
ABZ97695
ID ABZ97695 standard; DNA; 20 BP.
XX
AC ABZ97695;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human CCR3 oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; db.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

```

```

PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12937; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCCGCTC 17
Db 6 TTGCTCCGCTC 16

RESULT 15
ABD30726
ID ABD30726 standard; DNA; 20 BP.
XX
AC ABD30726;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human CCR3-derived oligonucleotide SEQ ID 12937.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense

```

PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 12937; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 52.4%; Score 11; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.8e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCCGCTC 17

DB 6 TTGCTCCGCTC 16

Search completed: September 12, 2005, 17:04:31

Job time : 175 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 14:04:18 ; Search time 174 Seconds
(without alignments)
714.452 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aacaaagagcgagcaacgaa 21

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2557800

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	12	ADP44613	Adp44613 Sense DNA
2	21	100.0	21	12	ADP44611	Adp44611 Sense DNA
C 3	19	90.5	21	12	ADP44614	Adp44614 Antisense
C 4	19	90.5	21	12	ADP44612	Adp44612 Antisense
C 5	12	57.1	25	9	AC135330	Ac135330 Human mic
6	11	52.4	19	12	ADK96972	Adk96972 Primer of
7	11	52.4	20	2	AA19405	Aax19405 Neurogeni
8	11	52.4	20	2	AAZ03368	Aaz03368 PCR prime
9	11	52.4	20	2	AAZ04279	Aaz04279 PCR prime
10	11	52.4	20	3	AAZ55953	Aaz55953 Xenopus l
C 11	11	52.4	20	4	AAF23328	Aaf23328 Oligonuc1
C 12	11	52.4	20	10	ADD56623	Add56623 Human gen
C 13	11	52.4	20	10	ABZ97696	Abz97696 Human CCR
C 14	11	52.4	20	10	ABZ97695	Abz97695 Human CCR
C 15	11	52.4	20	11	ABD30726	Abd30726 Human CCR
C 16	11	52.4	20	11	ABD30727	Abd30727 Human CCR
C 17	11	52.4	20	12	ADJ59552	Adj59552 Oligonuc1
C 18	11	52.4	20	12	ADJ59553	Adj59553 Oligonuc1
C 19	11	52.4	20	12	ADO45043	Ado45043 Human oli
C 20	11	52.4	20	12	ADO45042	Ado45042 Human oli

C 21	11	52.4	24	4	AAI69892	Aai69892 Human rib
C 22	11	52.4	25	6	ABQ87970	Abq87970 Enterohae
C 23	11	52.4	29	2	AAQ84819	Aaq84819 Spinocore
24	11	52.4	29	2	AAX80489	Aax80489 Human sec
25	11	52.4	29	4	AAS59324	Aas59324 Human sec
26	11	52.4	29	6	ABA90993	Aba90993 Biotinyla
27	11	52.4	29	12	ADO61037	Ado61037 Human deb
C 28	11	52.4	30	12	ADP80578	Adp80578 Novel mic
C 29	10	47.6	16	4	AAS00058	Aas00058 Synthetic
30	10	47.6	17	2	AAV42302	Aav42302 Primer us
C 31	10	47.6	17	2	AAV96406	Aav96406 Potato ci
C 32	10	47.6	17	2	AAV96405	Aav96405 Potato ci
C 33	10	47.6	17	6	ABS97488	Abs97488 Human epo
C 34	10	47.6	17	6	ACN01300	Acn01300 WNV Hamme
C 35	10	47.6	17	6	ACN12384	Acn12384 WNV minus
36	10	47.6	17	6	ACN14271	Acn14271 WNV minus
C 37	10	47.6	17	6	ACN04597	Acn04597 WNV Zinzy
38	10	47.6	17	6	ACN14270	Acn14270 WNV minus
C 39	10	47.6	17	6	ACN03280	Acn03280 WNV Inozy
C 40	10	47.6	17	6	ACN04596	Acn04596 WNV Zinzy
41	10	47.6	17	6	ACN12383	Acn12383 WNV minus
C 42	10	47.6	17	6	ACN01301	Acn01301 WNV Hamme
C 43	10	47.6	17	6	ACN03279	Acn03279 WNV Inozy
44	10	47.6	17	6	ACN09757	Acn09757 WNV minus
45	10	47.6	17	10	ADI49330	Adi49330 Human tum

ALIGNMENTS

RESULT 1
ADP44613
ID ADP44613 standard; DNA; 21 BP.
XX ADP44613;

XX 26-AUG-2004 (first entry)

Sense DNA 2 encoding an siRNA targeted to human ataxin 1 mRNA.

XX neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;

XX Huntington's; spinocerebellar ataxia type 1;

XX spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;

XX dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;

XX small interfering RNA; ss; human; ataxin 1.

XX Homo sapiens.

XX WO2004047872-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US037650.

XX 26-NOV-2002; 2002US-0429387P.

XX 03-FEB-2003; 2003US-0444614P.

XX (MEDT) MEDTRONIC INC.

XX Kaemmerer WF;

XX WPI; 2004-441106/41.

XX New medical system comprising an intracranial access device, a mapping means, a small interfering RNA or vector encoding the RNA, and a delivery means, useful for treating a neurodegenerative disorder.

XX Claim 68; SEQ ID NO 3; 228pp; English.

XX The invention relates to a novel medical system for treating a

XX neurodegenerative disorder comprising an intracranial access device, a

XX mapping means for locating a predetermined location in the brain, a

XX deliverable amount of a small interfering RNA (siRNA), or vector encoding

CC the siRNA, and a delivery means. The system of the invention has
CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the sense DNA 2 encoding an siRNA
CC targeted to human ataxin 1 mRNA of the invention.
XX
SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGAGCAACGAA 21
|||||
DB 1 AACCAAGAGCGGAGCAACGAA 21
|||||

RESULT 2
ADP44611
ID ADP44611 standard; DNA; 21 BP.
XX
AC ADP44611;
XX
DT 26-AUG-2004 (first entry)
XX
DE Sense DNA 1 encoding an siRNA targeted to human ataxin 1 mRNA.
XX
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
KW Huntington's; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
KW dentatorubral-pallidoluysian atrophy; DRPLA; siRNA;
KW small interfering RNA; ss; human; ataxin 1.
XX
OS Homo sapiens.
XX
PN WO2004047872-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037650.
XX
PR 26-NOV-2002; 2002US-0429387P.
PR 03-FEB-2003; 2003US-0444614P.
XX
PA (MEDT) MEDTRONIC INC.
XX
PI Kaemmerer WF;
XX
PT WPI; 2004-441106/41.
XX
PT New medical system comprising an intracranial access device, a mapping
PT means, a small interfering RNA or vector encoding the RNA, and a delivery
PT means, useful for treating a neurodegenerative disorder.
XX
PS Claim 68; SEQ ID NO 1; 228pp; English.
XX

CC The invention relates to a novel medical system for treating a
CC neurodegenerative disorder comprising an intracranial access device, a
CC mapping means for locating a predetermined location in the brain, a
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
CC the siRNA, and a delivery means. The system of the invention has
CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the sense DNA 1 encoding an siRNA
CC targeted to human ataxin 1 mRNA of the invention.
XX
SQ Sequence 21 BP; 10 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 21;

PD 16-SEP-2003.
 XX
 PF 08-MAR-2002; 2002JP-00064373.
 XX
 PR 08-MAR-2002; 2002JP-00064373.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2004-093977/10.
 XX
 PT Novel polynucleotide useful for PCR amplification along with two DNA
 PT fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.
 XX
 PS Claim 2; SEQ ID NO 6001; 2627pp; Japanese.
 XX
 CC The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.
 XX
 SQ Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 52.4%; Score 11; DB 12; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 AGAGCGGAGCA 16
 Db |||||
 5 AGAGCGGAGCA 15
 RESULT 7
 AAX19405
 ID AAX19405 standard; DNA; 20 BP.
 XX
 AC AAX19405;
 XX
 DT 19-MAY-1999 (first entry)
 XX
 DE Neurogenin protein PCR forward primer.
 KW Secreted protein; microsome; signal peptide; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9905256-A2.
 XX
 PD 04-FEB-1999.
 XX
 PF 24-JUL-1998; 98WO-US015394.
 XX
 PR 24-JUL-1997; 97US-0053586P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Kirschner MW, Kinoshita N;
 XX
 DR WPI; 1999-153316/13.
 XX
 PT Isolating nucleic acids encoding proteins comprising a signal peptide -
 PT by translating RNA and isolating translated RNA that is associated with
 PT microsomes, useful as therapeutic agents.
 XX
 PS Example 2; Page 34; 45pp; English.
 XX
 CC The present invention describes the isolation of nucleic acid (I) that
 CC encodes a protein (II) having a signal peptide (SP), which comprises
 CC isolating RNA molecules (III) that are associated with microsomes under
 CC conditions where (III) is at least partly translated. Also described are:
 CC (1) a library of (I) encoding (II) comprising SP; (2) (I) isolated by the
 CC above method; and (3) (II) encoded by (I). (I) and (II) are useful

CC therapeutically, typically (II) are cell growth factors such as
 CC cytokines, interleukins, colony-forming factors, possibly useful in
 CC treatment of cancer. (I) are also used: as tissue and molecular weight
 CC markers; as chromosome tags; to detect possible genetic disorders; as
 CC hybridisation probes to identify related nucleic acid; as primers for DNA
 CC fingerprinting; to generate antibodies; and in interaction trap assays to
 CC identify gene encoding specific binding agents. (II) are useful in drug
 CC screening, for raising antibodies (e.g. for use as immunoassay reagents)
 CC and to induce an immune response. The method is more efficient and
 CC reliable than the sequence trap system. It does not involve formation of
 CC a fusion protein (rather natural proteins are selected) and (II) do not
 CC have to be secreted. The present sequence represents a PCR primer which
 CC is used in an example from the present invention
 XX
 SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 52.4%; Score 11; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CAAGAGCGGAG 14
 Db |||||
 1 CAAGAGCGGAG 11
 RESULT 8
 AAZ03368
 ID AAZ03368 standard; DNA; 20 BP.
 XX
 AC AAZ03368;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritendinitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX
 PN WO9928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB001939.
 XX
 PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-371125/31.
 XX
 PT Genome sequence of Chlamydia trachomatis.
 XX
 PS Disclosure; Page 1601; 1755pp; English.
 XX
 CC PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,
 CC epididymitis, cervicitis, salpingitis, peritendinitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.

CC The polypeptides of the invention may be of use in treating these

XX diseases

SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 52.4%; Score 11; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGAGCAACGAA 21

|||||

Db 2 GGAGCAACGAA 12

RESULT 9

AAZ04279

ID AAZ04279 standard; DNA; 20 BP.

XX

AC AAZ04279;

XX

DT 07-OCT-1999 (first entry)

XX

DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX

OS Synthetic.

OS Chlamydia trachomatis.

XX

PN WO928475-A2.

XX

PD 10-JUN-1999.

XX

PF 27-NOV-1998; 98WO-IB001939.

XX

PR 28-NOV-1997; 97FR-00015041.

XX

PR 17-DEC-1997; 97FR-00016034.

XX

PR 04-NOV-1998; 98US-0107077P.

XX

PA (GEST) GENSET.

XX

PI Griffais R;

XX

DR WPI; 1999-371125/31.

XX

PT Genome sequence of Chlamydia trachomatis.

XX

PS Disclosure; Page 1675; 1755pp; English.

XX

CC PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

XX

SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match

Best Local Similarity 52.4%; Score 11; DB 2; Length 20;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGGAGCAACGA 20

|||||

Db 5 CGGAGCAACGA 15

RESULT 10

AAZ55953

ID AAZ55953 standard; cDNA; 20 BP.

XX

AC AAZ55953;

XX

DT 10-APR-2000 (first entry)

XX

DE Xenopus laevis neurogenin sense PCR primer, SEQ ID NO:31.

XX

KW Neurogenin; Zic3; zinc finger; neuroregeneration; neurological disease;
 KW diagnosis; Alzheimer's disease; expression pattern; PCR primer; ss.

XX

OS Xenopus laevis.

XX

PN JP11341985-A.

XX

PD 14-DEC-1999.

XX

PF 30-APR-1998; 98JP-00121456.

XX

PR 31-MAR-1998; 98JP-00086979.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

DR WPI; 2000-101694/09.

XX

PT A nerve formation-inducing gene - useful as a diagnostic agent for
 PT nervous diseases, and for treating Alzheimer disease.

XX

PS Example 2; Page 14; 30pp; Japanese.

XX

CC The invention relates to Xenopus laevis Zic3 protein (AA69524). Zic3
 CC contains a zinc finger motif, and induces the formation of neurons. The
 CC cDNA was obtained from embryonic Xenopus nerve poly(A+) RNA. Zic3, and
 CC nucleotides encoding it, are useful as diagnostic tools for neurological
 CC diseases, and for the treatment of Alzheimer's disease. Sequences
 CC AAZ55931-Z55962 represent PCR primers used to determine which other genes
 CC are expressed with Zic3 in various Xenopus cell types in an
 CC exemplification of the present invention

XX

SQ Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 52.4%; Score 11; DB 3; Length 20;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 CAAGAGCGGAG 14

Db

1 CAAGAGCGGAG 11

RESULT 11

AAZ23328/c

ID AAZ23328 standard; DNA; 20 BP.

XX

AC AAZ23328;

XX

DT 19-MAR-2001 (first entry)

XX

DE Oligonucleotide for detection of Mycobacterium porcinum.

XX

KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;
 KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
 KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
 KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
 KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.

XX

OS Mycobacterium porcinum.

XX

PN WO200073436-A1.
 XX 07-DEC-2000.
 XX 16-MAY-2000; 2000WO-KR000477.
 XX 29-MAY-1999; 99KR-00019631.
 XX 29-MAY-1999; 99KR-00019632.
 XX 29-MAY-1999; 99KR-00019633.
 XX 29-MAY-1999; 99KR-00019634.
 XX 29-MAY-1999; 99KR-00019635.
 XX 07-APR-2000; 2000KR-00018189.
 XX (SJHI-) SJ HIGHTECH CO LTD.
 PA (KIMC/) KIM C M.
 PA (KIMC/) PARK H K.
 XX Kim CM, Park HK, Jang HJ;
 XX WPI; 2001-061527/07.
 XX Novel oligonucleotide sequences of internal transcribing spacer region of
 PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
 PT detecting and identifying mycobacteria and distinguish TB complex from
 PT NTM.
 XX Claim 34; Page 78; 89pp; English.
 XX The present sequence is an oligonucleotide developed using a
 CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
 CC sequence. ITS DNA sequences from *M. fortuitum*, *M. chelonae*, *M. abscessus*,
 CC *M. vaccae*, *M. flavescens*, *M. asiaticum*, *M. porcinum*, *M. acapulcensis*, *M.*
 CC *thermophiles* genes were identified. The oligonucleotides derived from
 CC these sequences were used to develop PCR primers and hybridisation probes
 CC for detection and identification of Mycobacterium. ITS has a more
 CC polymorphic region than 16S rRNA and also has a conserved region. It is
 CC therefore highly effective as a target DNA for distinction of genotype.
 CC The oligonucleotide probes, attached to solid substrate, hybridise only
 CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
 CC can detect and identify the specific mycobacteria sensitively. The
 CC oligonucleotides can also detect and identify the specific mycobacteria
 CC by PCR amplification. Using the oligonucleotide primers or probes made
 CC from ITS of mycobacteria, it is possible to detect mycobacteria,
 CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
 CC (NTM), and to identify mycobacteria species accurately and effectively
 XX
 XX Sequence 20 BP; 0 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 52.4%; Score 11; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 AGCGGAGCAAC 18
 DB 20 AGCGGAGCAAC 10
 RESULT 12
 ADD56623/C
 ID ADD56623 standard; DNA; 20 BP.
 XX
 AC ADD56623;
 XX 15-JAN-2004 (first entry)
 XX Human gene expression analysis multiplex Start-PCR primer #143.
 XX Gene expression; multiplex standardised reverse transcriptase-PCR;
 KW Start-PCR; high density oligonucleotide array; cDNA array;
 KW small biological sample; fine needle aspirate biopsy;
 KW laser captured microdissected material; human; primer; ss.
 XX Homo sapiens.
 OS

XX US2003186246-A1.
 PN 02-OCT-2003.
 XX 28-MAR-2002; 2002US-00109349.
 XX 28-MAR-2002; 2002US-00109349.
 XX (WILL/) WILLEY J C.
 PA (CRAW/) CRAWFORD E L.
 XX Willey JC, Crawford EL;
 XX WPI; 2003-811730/76.
 DR Direct comparison of numerical gene expression values between samples of
 XX genes comprises using multiplex standardized reverse transcription-
 PT polymerase chain reaction.
 XX Example 1; SEQ ID NO 143; 59pp; English.
 XX The present invention relates to a method for the direct comparison of
 CC numerical gene expression values between samples of genes. The method
 CC comprises amplifying cDNA in the presence of a competitive template
 CC mixture and primer pairs for several genes and then amplifying aliquots
 CC of the PCR products using a primer pair specific for each gene. The
 CC method of amplification is by multiplex standardised reverse
 CC transcriptase-polymerase chain reaction (Start-PCR). High density
 CC oligonucleotide or cDNA arrays are used to measure PCR products following
 CC quantitative Start-PCR. The method is useful for the assessment of gene
 CC expression in small biological samples such as fine needle aspirate
 CC biopsies, and laser captured microdissected materials. The method allows
 CC for the standardised measurement of hundreds of genes from the same
 CC sample, which in prior art, could only be assessed for one gene. The
 CC present sequence represents a multiplex Start-PCR primer which can be
 CC used in the method of the present invention.
 XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 52.4%; Score 11; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGAGCAACGAA 21
 DB 18 GGAGCAACGAA 8
 RESULT 13
 ABZ97696/C
 ID ABZ97696 standard; DNA; 20 BP.
 XX
 AC ABZ97696;
 XX 17-OCT-2003 (first entry)
 XX Human CCR3 oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 OS
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 PF

```
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12938; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
XX
Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GAGCGGAGCAA 17
DB 11 GAGCGGAGCAA 1
XX
RESULT 14
ABZ97695/c
XX ID ABZ97695 standard; DNA; 20 BP.
XX AC ABZ97695;
XX XX
XX DT 17-OCT-2003 (first entry)
XX DE Human CCR3 oligonucleotide sequence.
XX XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX KW lung inflammation; respiratory disease; ds.
XX XX
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX XX
XX PD 31-OCT-2002.
XX XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12937; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 52.4%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GAGCGGAGCAA 17
DB 16 GAGCGGAGCAA 6
XX
RESULT 15
ABD30726/c
XX ID ABD30726 standard; DNA; 20 BP.
XX AC ABD30726;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Human CCR3-derived oligonucleotide SEQ ID 12937.
XX XX
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX KW pulmonary transplantation rejection; ss; primer.
XX XX
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX XX
XX PD 31-OCT-2002.
XX XX
```

XX 23-APR-2002; 2002WO-US013143.
 PF
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 XX WPI; 2003-093058/08.
 DR
 XX
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 PT
 XX Claim 15; SEQ ID NO 12937; 763pp; English.
 PS
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 XX SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 52.4%; Score 11; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GAGCGGAGCAA 17
 Db 16 GAGCGGAGCAA 6
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Search completed: September 12, 2005, 17:04:30
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005., 16:58:36 ; Search time 278.5 Seconds
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SUMMARIES

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4	21	100.0	21	20	US-10-852-997-3
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c	8	19	90.5	21	20	US-10-852-997-4	Sequence 4, Appli
c	9	13	61.9	25	21	US-10-809-189-18110	Sequence 18110, A
c	10	13	61.9	25	21	US-10-809-189-18111	Sequence 18111, A
c	11	13	61.9	25	22	US-10-719-956-201094	Sequence 201094, A
c	12	13	61.9	25	22	US-10-719-956-425371	Sequence 425371, A
c	13	12	57.1	25	15	US-10-098-263B-35321	Sequence 35321, A
c	14	12	57.1	25	21	US-10-719-900-49468	Sequence 49468, A
c	15	12	57.1	25	21	US-10-719-900-272193	Sequence 272193, A
c	16	12	57.1	25	21	US-10-719-900-399511	Sequence 399511, A
c	17	12	57.1	25	21	US-10-719-900-548718	Sequence 548718, A
c	18	12	57.1	25	21	US-10-719-900-911843	Sequence 911843, A
c	19	12	57.1	25	21	US-10-719-900-911844	Sequence 911844, A
c	20	12	57.1	25	21	US-10-719-900-950357	Sequence 950357, A
c	21	12	57.1	25	21	US-10-719-900-978443	Sequence 978443, A
c	22	12	57.1	25	21	US-10-956-157-278869	Sequence 278869, A
c	23	12	57.1	25	22	US-10-719-956-202563	Sequence 202563, A
c	24	12	57.1	25	22	US-10-719-956-573056	Sequence 573056, A
c	25	11	52.4	20	15	US-10-244-367-31	Sequence 31, Appli
c	26	11	52.4	20	16	US-10-109-349A-143	Sequence 143, Appl
c	27	11	52.4	20	17	US-10-448-836-202	Sequence 202, App
c	28	11	52.4	20	17	US-10-448-914A-202	Sequence 202, App
c	29	11	52.4	21	20	US-10-751-736-14580	Sequence 14580, A
c	30	11	52.4	21	20	US-10-751-736-19971	Sequence 19971, A
c	31	11	52.4	21	20	US-10-751-736-20001	Sequence 20001, A
c	32	11	52.4	21	20	US-10-751-736-46366	Sequence 46366, A
c	33	11	52.4	21	20	US-10-751-736-46367	Sequence 46367, A
c	34	11	52.4	22	21	US-10-933-611-11	Sequence 11, Appl
c	35	11	52.4	22	21	US-10-933-611-12	Sequence 12, Appl
c	36	11	52.4	22	21	US-10-933-611-15	Sequence 15, Appl
c	37	11	52.4	22	21	US-10-933-611-16	Sequence 16, Appl
c	38	11	52.4	25	19	US-10-250-997-69	Sequence 69, Appl
c	39	11	52.4	25	21	US-10-719-900-142642	Sequence 142642, A
c	40	11	52.4	25	21	US-10-719-900-206389	Sequence 206389, A
c	41	11	52.4	25	21	US-10-719-900-248436	Sequence 248436, A
c	42	11	52.4	25	21	US-10-719-900-256115	Sequence 256115, A
c	43	11	52.4	25	21	US-10-719-900-290010	Sequence 290010, A
c	44	11	52.4	25	21	US-10-719-900-297061	Sequence 297061, A
c	45	11	52.4	25	21	US-10-719-900-297062	Sequence 297062, A

ALIGNMENTS

RESULT 1
US-10-721-693-1
; Sequence 1, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-1

Query Match 100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGAGCAACGAA 21
|||||
Db 1 AACCAAGAGCGGAGCAACGAA 21

RESULT 2

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US-10-721-693-3
; Sequence 3, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-3
Query Match      100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
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RESULT 3
US-10-852-997-1
; Sequence 1, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-1
Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
|||||
RESULT 4
US-10-852-997-3
; Sequence 3, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
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US-10-721-693-3
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-3
Query Match      100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACCAAGAGCGGAGCAACGAA 21
Db      1 AACCAAGAGCGGAGCAACGAA 21
|||||
RESULT 5
US-10-721-693-2/c
; Sequence 2, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-2
Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 CCAAGAGCGGAGCAACGAA 21
Db      21 CCAAGAGCGGAGCAACGAA 3
|||||
RESULT 6
US-10-721-693-4/c
; Sequence 4, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-721-693-4
Query Match      90.5%; Score 19; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 CCAAGAGCGGAGCAACGAA 21
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Db 21 CCAAGAGCGGAGCAACGAA 3
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RESULT 7
US-10-852-997-2/c
; Sequence 2, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; PRIOR FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-2
Query Match 90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAAGAGCGGAGCAACGAA 21
|||||
Db 21 CCAAGAGCGGAGCAACGAA 3

RESULT 8
US-10-852-997-4/c
; Sequence 4, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR FILING DATE: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-997-4
Query Match 90.5%; Score 19; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAAGAGCGGAGCAACGAA 21
|||||
Db 21 CCAAGAGCGGAGCAACGAA 3

RESULT 9
US-10-809-189-18110/c
; Sequence 18110, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
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; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18110
Query Match 61.9%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGA 13
|||||
Db 21 AACCAAGAGCGGA 9

RESULT 10
US-10-809-189-18111/c
; Sequence 18111, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18111
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18111
Query Match 61.9%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGA 13
|||||
Db 13 AACCAAGAGCGGA 1

RESULT 11
US-10-719-956-201094/c
; Sequence 201094, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
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; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 201094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-201094

Query Match      61.9%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGGA 13
Db 16 AACCAAGAGCGGA 4

RESULT 12
US-10-719-956-425371
; Sequence 425371, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 425371
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-425371

Query Match      61.9%; Score 13; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACCAAGAGCGGAG 14
Db 12 ACCAAGAGCGGAG 24

RESULT 13
US-10-098-263B-35321/c
; Sequence 35321, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35321

Query Match      57.1%; Score 12; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGCGG 12

RESULT 14
US-10-719-900-49468
; Sequence 49468, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-49468

Query Match      57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGAGCGGAGCAA 17
Db 10 AGAGCGGAGCAA 21

RESULT 15
US-10-719-900-272193/c
; Sequence 272193, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 272193
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-272193

Query Match      57.1%; Score 12; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAGAGCGGAGCA 16
Db 15 AAGAGCGGAGCA 4

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Job time : 279.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 16:40:43 ; Search time 58 Seconds
(without alignments)
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Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aaccaagagcgagcaacgaa 21

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Gapop_60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 914340

Minimum DB seq length: 15

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 4	11	52.4	20	3	US-09-172-045-31
c 5	11	52.4	20	4	US-09-342-325C-31
c 6	11	52.4	20	4	US-09-380-052-202
c 7	11	52.4	22	4	US-09-332-522B-81
c 8	11	52.4	25	4	US-09-396-196G-14051
c 9	11	52.4	25	4	US-09-396-196G-18094
c 10	11	52.4	25	4	US-09-396-196G-18109
c 11	11	52.4	25	4	US-09-396-196G-66426
c 12	11	52.4	25	4	US-09-396-196G-66427
c 13	11	52.4	25	4	US-09-396-196G-66438
c 14	11	52.4	29	2	US-08-267-803B-81
c 15	11	52.4	30	3	US-08-848-810-42
c 16	10	47.6	16	3	US-09-648-040-8
c 17	10	47.6	16	4	US-09-371-772B-5859
c 18	10	47.6	17	4	US-09-319-265-5
c 19	10	47.6	17	4	US-09-371-772B-4854
c 20	10	47.6	17	4	US-09-371-772B-4855
c 21	10	47.6	18	3	US-09-344-521-22
c 22	10	47.6	19	3	US-09-360-416-81
c 23	10	47.6	20	2	US-08-860-882A-46
c 24	10	47.6	20	3	US-08-875-223-3
c 25	10	47.6	20	3	US-09-011-769A-28
c 26	10	47.6	20	4	US-09-422-978-10903
c 27	10	47.6	20	4	US-09-198-452A-5309

c 28	10	47.6	20	4	US-09-198-452A-5528	Sequence 5528, Ap
c 29	10	47.6	20	4	US-09-198-452A-5645	Sequence 5645, Ap
c 30	10	47.6	20	4	US-09-198-452A-5646	Sequence 5646, Ap
c 31	10	47.6	20	4	US-09-922-146-11	Sequence 11, Appl
c 32	10	47.6	20	4	US-10-023-649A-19	Sequence 19, Appl
c 33	10	47.6	21	3	US-09-210-896-22	Sequence 22, Appl
c 34	10	47.6	22	3	US-08-793-044-7	Sequence 7, Appl
c 35	10	47.6	22	5	PCT-US93-12078-2	Sequence 2, Appl
c 36	10	47.6	22	5	PCT-US93-12078-3	Sequence 3, Appl
c 37	10	47.6	23	2	US-08-210-762B-63	Sequence 63, Appl
c 38	10	47.6	23	3	US-09-106-075A-63	Sequence 63, Appl
c 39	10	47.6	23	3	US-09-102-831-16	Sequence 16, Appl
c 40	10	47.6	24	2	US-08-210-762B-65	Sequence 65, Appl
c 41	10	47.6	24	3	US-09-284-900-2	Sequence 2, Appl
c 42	10	47.6	24	3	US-09-106-075A-65	Sequence 65, Appl
c 43	10	47.6	24	4	US-09-270-767-62514	Sequence 62514, A
c 44	10	47.6	25	1	US-08-379-926A-4	Sequence 4, Appl
c 45	10	47.6	25	4	US-09-396-196G-7356	Sequence 7356, Ap

ALIGNMENTS

RESULT 1
US-09-396-196G-18110/c
; Sequence 18110, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18110

Query Match 61.9%; Score 13; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGCGGGA 13
Db 21 AACCAAGCGGGA 9

RESULT 2
US-09-396-196G-18111/c
; Sequence 18111, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18111


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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium porcinum
US-09-980-052-202

Query Match      52.4%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AGCGGAGCAAC 18
      |||||
Db      20 AGCGGAGCAAC 10

RESULT 7
US-09-332-522E-81/c
; Sequence 81, Application US/09332522E
; Patent No. 6781028
; GENERAL INFORMATION:
; APPLICANT: Costa, M.
; APPLICANT: Doberstein, S.
; APPLICANT: Elson, S.
; APPLICANT: Ferguson, K.
; APPLICANT: Homburger, S.
; TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND S
; FILE REFERENCE: 7326-101, EX99-004
; CURRENT APPLICATION NUMBER: US/09/332,522E
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-332-522E-81

Query Match      52.4%; Score 11; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GGAGCAACGAA 21
      |||||
Db      22 GGAGCAACGAA 12

RESULT 8
US-09-396-196G-14051
; Sequence 14051, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14051

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCAAGAGCGGA 13
      |||||
Db      25 CCAAGAGCGGA 15

RESULT 11
```

```
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCAAGAGCGGA 13
      |||||
Db      7 CCAAGAGCGGA 17

RESULT 9
US-09-396-196G-18094/c
; Sequence 18094, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18094

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCAAGAGCG 11
      |||||
Db      11 AACCAAGAGCG 1

RESULT 10
US-09-396-196G-18109/c
; Sequence 18109, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18109

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 CCAAGAGCGGA 13
      |||||
Db      25 CCAAGAGCGGA 15

RESULT 11
```

```
US-09-396-196G-66426
; Sequence 66426, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66426

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GAGCGGAGCAA 17
        |||||
Db      14 GAGCGGAGCAA 24

RESULT 12
US-09-396-196G-66427
; Sequence 66427, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66427

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GAGCGGAGCAA 17
        |||||
Db      12 GAGCGGAGCAA 22

RESULT 13
US-09-396-196G-66438
; Sequence 66438, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66438

Query Match      52.4%; Score 11; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCAAGAGCG 11
        |||||
US-08-267-803B-81

Query Match      52.4%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GAGCGGAGCAA 17
        |||||
Db      10 GAGCGGAGCAA 20

RESULT 14
US-08-267-803B-81
; Sequence 81, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 591415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-267-803B-81

Query Match      52.4%; Score 11; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AACCAAGAGCG 11
        |||||
```

Db 19 AACCAAGAGCG 29

RESULT 15
US-08-848-810-42
; Sequence 42, Application US/08848810
; Patent No. 6074851
; GENERAL INFORMATION:
; APPLICANT: Deibel Jr., M. R.
; APPLICANT: Yem, A. W.
; APPLICANT: Wilson, C. L.
; TITLE OF INVENTION: Catalytic Macro Molecules Having DCD25B
; TITLE OF INVENTION: Like Activity
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn Company
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,810
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-833-7914
; TELEFAX: 616-833-6897
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-848-810-42

Query Match 52.4%; Score 11; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAGCGGAGCAA 17
|||||
Db 4 GAGCGGAGCAA 14

Search completed: September 12, 2005, 18:11:00
Job time : 60 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 15:58:45 ; Search time 1377.5 Seconds
(without alignments)
580.290 Million cell updates/sec

Title: US-10-721-693-1

Perfect score: 21

Sequence: 1 aaccaagagcggaacgaa 21

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 42690

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	47.6	25	9	CG712540 1119027E0
C 2	10	47.6	28	7	R60473 yhl3g06.r1
C 3	10	47.6	30	9	AG201067 Pan trogl
C 4	9	42.9	19	8	AZ599480 1M0414C20
C 5	9	42.9	20	9	AJ593450 Arabidops
C 6	9	42.9	25	4	BM399181 5009-0-54
C 7	9	42.9	28	9	AG203460 Pan trogl
C 8	9	42.9	30	8	AZ861916 2M0168K17
C 9	8	38.1	17	9	AJ598448 Arabidops
C 10	8	38.1	18	4	BM398577 5009-0-47
C 11	8	38.1	20	1	AU256829 AU256829
C 12	8	38.1	20	4	BM397580 5009-0-34
C 13	8	38.1	20	4	BM398685 5009-0-48
C 14	8	38.1	20	4	BM398964 5009-0-51
C 15	8	38.1	20	4	BM398968 5009-0-51
C 16	8	38.1	20	8	AZ637794 1M0497D20
C 17	8	38.1	20	8	AZ766411 1M0564B02
C 18	8	38.1	20	8	AZ834769 2M0117F08
C 19	8	38.1	21	4	BM397402 5009-0-32
C 20	8	38.1	21	4	BM398994 5009-0-51
C 21	8	38.1	21	8	AZ636817 1M0495C20
C 22	8	38.1	21	9	AG190199 Pan trogl
C 23	8	38.1	22	1	A1723177 fc33f01.x
C 24	8	38.1	22	1	AU257837 AU257837

25	8	38.1	22	4	BM398612	5009-0-47
26	8	38.1	22	4	BM399170	5009-0-54
27	8	38.1	22	8	AZ326642	1M0049D09
28	8	38.1	22	8	AZ423444	1M0202J03
C 29	8	38.1	22	8	AZ829837	2M0107P11
30	8	38.1	23	4	BM398108	5009-0-40
31	8	38.1	23	4	BM398156	5009-0-41
32	8	38.1	23	4	BM400852	5009-0-8-
33	8	38.1	23	8	AZ593454	1M0405C03
C 34	8	38.1	23	8	AZ822792	2M0096015
35	8	38.1	24	4	BM396198	5009-0-18
36	8	38.1	24	4	BM399525	5009-0-58
37	8	38.1	24	4	BM399548	5009-0-59
38	8	38.1	24	7	CF311108	ABF--06-D
C 39	8	38.1	24	8	AZ468735	1M0281I14
C 40	8	38.1	24	8	AZ491197	1M0324C10
C 41	8	38.1	24	8	AZ502375	1M0341F08
C 42	8	38.1	24	8	AZ859121	2M0164A07
C 43	8	38.1	25	1	AU256438	AU256438
C 44	8	38.1	25	4	BM399155	5009-0-54
45	8	38.1	25	4	BM399247	5009-0-55

ALIGNMENTS

CG712540 25 bp DNA linear GSS 20-OCT-2003
1119027E01.2EL_y2 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.

CG712540 GI:37738446

GSS.

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 25)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119027 row: E column: 01

Class: transposon-tagged.

Location/Qualifiers

source

1. 25

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pluScript backbone); Site:1: BamHI; Site:2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA

was extracted from leaf strips, double digested using

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 47.6%; Score 10; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGACGGAGC 15
|||||
Db 11 AGACGGAGC 20

RESULT 2

R60473/c 28 bp mRNA linear EST 24-MAY-1995
LOCUS
DEFINITION
vhl3q06.r1 Soares infant brain IN1B Homo sapiens cDNA clone
IMAGE:43057 5' similar to SP:SYNP_RAT P22831 ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
R60473.1 GI:831168
Homo sapiens (human)

REFERENCE
AUTHORS
1 (bases 1 to 28)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Ruchling, T., Soares, M., Tan, P.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
JOURNAL
COMMENT
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1

Source: IMAGE Consortium LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand

Seq primer: M13RP1

High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:415598"
/db_xref="taxon:9606"
/clone="IMAGE:43057"
/sex="female"

/dev stage="73 days post natal"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain IN1B"
/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AAGTGAAGAAATTCGGCGCGAGGAAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaudo."

ORIGIN

Query Match 47.6%; Score 10; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 AGCGGAGCAA 17
|||||
Db 24 AGCGGAGCAA 15

RESULT 3

AG201067/c 30 bp DNA linear GSS 06-MAR-2004
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-083G08.TJ, genomic survey
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AG201067.1 GI:45233242
GSS.
Pan troglodytes (chimpanzee)

REFERENCE
AUTHORS
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

2 (bases 1 to 30)
Unpublished
BAC end sequences of Library RP-43
Pan troglodytes (chimpanzee)

REFERENCE
AUTHORS
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

2 (bases 1 to 30)
Unpublished
BAC end sequences of Library RP-43
Pan troglodytes (chimpanzee)

COMMENT
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS
Sequencing: TJ

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..30
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-083G08.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 47.6%; Score 10; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACCAAGAGC 10
|||||
Db 29 AACCAAGAGC 20

RESULT 4

AZ599480 19 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
1M0414C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0414C20 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ599480.1 GI:11721670
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
1
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0414 row: C column: 20
 Seq primer: CACACGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
FEATURES
 source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0414C20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 42.9%; Score 9; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGCGGAGC 15
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 Db 8 GAGCGGAGC 16

RESULT 5
 AJ593450/c 20 bp DNA linear GSS 15-JAN-2004
LOCUS
 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 380F06, genomic survey sequence.
DEFINITION
 Arabidopsis thaliana T-DNA flanking sequence.
ACCESSION
 AJ593450
VERSION
 AJ593450.1 GI:37943074
KEYWORDS
 GSS; left border; T-DNA flanking sequence.
SOURCE
 Arabidopsis thaliana (thale cress)
ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Query Match 42.9%; Score 9; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCAACGA 20
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 Db 10 GAGCAACGA 2

RESULT 6
 BM399181 25 bp mRNA linear EST 17-JAN-2002
LOCUS
 Tetrahymena thermophila CDNA (large fraction)
DEFINITION
 Tetrahymena thermophila CDNA, mRNA sequence.
ACCESSION
 BM399181
VERSION
 BM399181.1 GI:18199234
KEYWORDS
 EST
SOURCE
 Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
 1 (bases 1 to 25)
REFERENCE
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.
AUTHORS
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
TITLE
 Contact: Turkewitz AP
JOURNAL
 Molecular Genetics and Cell Biology
COMMENT
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
REFERENCE
AUTHORS
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, P.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
JOURNAL
 EMBO Rep. 3 (12), 1152-1157 (2002)
COMMENT
 22363535
 12446565
 2 (bases 1 to 20)
 Balzerque, S.
REFERENCE
AUTHORS
 Direct Submission
TITLE
 Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
JOURNAL
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (http://www.genoplante.com and
 http://genoplante-info.infobiogen.fr).
FEATURES
 Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassilewskija"
 /db_xref="taxon:3702"
 /clone="380F06"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 misc_feature
 1..20
 /note="T-DNA flanking sequence
 left border"

Seq primer: T3.		Location/Qualifiers		Db	
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/mol_type="mRNA"		/strain="CU428.1"			
/db_xref="taxon:5911"		/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"		AZ861916	
/notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."		42.9%; Score 9; DB 4; Length 25;		2M0168K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic	
Best Local Similarity 100.0%; Pred. No. 6.5e+05;		0; Mismatches 0; Indels 0; Gaps 0;		clone UUGC2M0168K17 R, genomic survey sequence.	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		7 GAGCGGAGC 15		AZ861916	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		AZ861916.1 GI:13058714	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		GSS.	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Mus musculus (house mouse)	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Mus musculus	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		1 (bases 1 to 30)	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Niederhausern,A. and Wright,D., Weiss,R.	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Mouse whole genome scaffolding with paired end reads from 10kb	
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1 GAGCGGAGC 9		1 GAGCGGAGC 9		Unpublished (2000)	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Contact: Robert B. Weiss	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		University of Utah Genome Center	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		University of Utah	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		84112, USA	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Tel: 801 585 5606	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Fax: 801 585 7177	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Email: ddunn@genetics.utah.edu	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Insert Length: 10000 Std Error: 0.00	
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1 GAGCGGAGC 9		1 GAGCGGAGC 9		/notes="Vector: PWD42nv; Purified genomic DNA from M.	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		musculus C57BL/6J (male) was obtained from the Jackson	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Laboratory Mouse DNA Resource	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		(http://www.jax.org/resources/documents/dnares/). The DNA	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		was hydrodynamically sheared by repeated passage through a	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		0.005 inch orifice at constant velocity. The sheared DNA	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		was blunt end-repaired with T4 DNA polymerase and T4	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		ligated to the blunt ends in high molar excess. The	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		polynucleotide kinase. Adaptor oligonucleotides were	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		ligated to the blunt ends in high molar excess. The	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		adaptor DNA was purified and size-selected for a 9.5 to	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		10.5 kb range using preparative agarose gel	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		electrophoresis. Vector DNA was prepared from a derivative	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		of PWD42 (g14732114[gb AF129072.1]), a copy-number	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		inducible derivative of plasmid R1. The vector was ligated	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		with adaptors complementary to the insert adaptors and	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		purified. The sheared, adaptor mouse DNA was annealed to	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		adaptor vector DNA, and transformed into	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		chemically-competent E. coli XL10-Gold (Stratagene) cells	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		and selected for ampicillin resistance."	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		42.9%; Score 9; DB 8; Length 30;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Query Match	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Best Local Similarity 100.0%; Pred. No. 6.5e+05;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		7 GAGCGGAGC 15	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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1 GAGCGGAGC 9		1 GAGCGGAGC 9		9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db          |||||
9 GAGCGGAGC 17

RESULT 9
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LOCUS      17 bp      DNA      linear      GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
468F11, genomic survey sequence.
ACCESSION  AJ598448
VERSION     1 GI:37948076
KEYWORDS   GSS; right border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE  1
AUTHORS    Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, P.,
            Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
            Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE      T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL    EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE    22363535
PUBMED     1246565
REFERENCE  2 (bases 1 to 17)
AUTHORS    Balzerque, S.
TITLE      Direct Submission
JOURNAL    Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT    PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infoibioen.fr).

FEATURES   source
            1..17
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            /db_xref="taxon:3702"
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            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            misc_feature 1..17
            /note="T-DNA flanking sequence
            right border"

ORIGIN
Query Match      38.1%; Score 8; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACCAAGA 8
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Db 16 AACCAAGA 9

RESULT 10
BM398577
LOCUS      18 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM398577
VERSION     1 GI:18198630
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila

FEATURES   source
            1..20
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
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ORIGIN
Query Match      38.1%; Score 8; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;

ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
            Frankel, J. and Klobutcher, L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Unpublished (2002)
COMMENT    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3
            Location/Qualifiers
                1..18
                /organism="Tetrahymena thermophila"
                /mol_type="mRNA"
                /strain="CU428.1"
                /db_xref="taxon:5911"
                /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                /note="Vector: Bluescript SK+; Details on library
                preparation can be found in Chilcoat and Turkewitz (2001)
                Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%; Score 8; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGCGGAGC 15
    |||||
Db 4 AGCGGAGC 11

RESULT 11
AU256829/c
LOCUS      20 bp      mRNA      linear      EST 25-APR-2002
DEFINITION AU256829 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0009047 3', mRNA sequence.
ACCESSION  AU256829
VERSION     1 GI:20320851
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kato, K. and Matoba, R.
TITLE      Generation of expressed sequence tags from mouse brain
JOURNAL    Unpublished (2002)
COMMENT    Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkatoba@nara.ac.jp,
            URL: http://love2.aist-nara.ac.jp/BED/index.html.
            Location/Qualifiers
                1..20
                /organism="Mus musculus"
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                /clone="BED003047"
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ORIGIN
Query Match      38.1%; Score 8; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+06;

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Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY          2  ACCAAG  9
            |||||
Db          17  ACCAAG  10

RESULT 12
BM397580      20 bp  mRNA      linear      EST 17-JAN-2002
LOCUS      5009-0-34-G11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION  Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM397580
VERSION     BM397580.1  GI:18197633
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
ORGANISM    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
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                     /organism="Tetrahymena thermophila"
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                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Best Local Similarity 100.0%;  Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY          8  AGCGGAGC 15
            |||||
Db          3  AGCGGAGC 10

RESULT 14
BM398964      20 bp  mRNA      linear      EST 17-JAN-2002
LOCUS      5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION  Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398964
VERSION     BM398964.1  GI:18199017
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
ORGANISM    Eukaryota; Alveolata; Ciliophora; Oligohymenophores;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
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                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY          8  AGCGGAGC 15
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Db          2  AGCGGAGC  9

RESULT 13
BM398685      20 bp  mRNA      linear      EST 17-JAN-2002
LOCUS      5009-0-48-G09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION  Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398685
VERSION     BM398685.1  GI:18198738
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
ORGANISM    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago

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920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES             Location/Qualifiers
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                     /note="Vector: Bluescript2 SK+; Details on library
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                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%;  Score 8;  DB 4;  Length 20;
Best Local Similarity 100.0%;  Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY          8  AGCGGAGC 15
            |||||
Db          3  AGCGGAGC 10

RESULT 14
BM398964      20 bp  mRNA      linear      EST 17-JAN-2002
LOCUS      5009-0-51-B10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION  Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398964
VERSION     BM398964.1  GI:18199017
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
ORGANISM    Eukaryota; Alveolata; Ciliophora; Oligohymenophores;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
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                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      38.1%;  Score 8;  DB 4;  Length 20;
Best Local Similarity 100.0%;  Pred. No. 2.6e+06;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY          8  AGCGGAGC 15
            |||||
Db          2  AGCGGAGC  9

RESULT 15

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BM398968
LOCUS 20 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-51-C03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398968
VERSION BM398968
KEYWORDS GI:18199021
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 20)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
source Location/Qualifiers
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/organism="Tetrahymena thermophila"
/mol_type="mRNA"
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 15

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Post-processing: Listing first 45 summaries

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13: gb_un.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	CQ824575 Sequence
2	21	100.0	21	6	CQ824577 Sequence
3	19	90.5	21	6	CQ824574 Sequence
4	19	90.5	21	6	CQ824576 Sequence
5	12	57.1	22	6	AR568156 Sequence
6	12	57.1	30	6	AX463675 Sequence
7	11	52.4	20	6	E30575 Sequence
8	11	52.4	20	6	AR268863 Sequence
9	11	52.4	20	6	AR442594 Sequence
10	11	52.4	30	6	AR098219 Sequence
11	11	52.4	30	6	BD195066 Catalytic
12	11	52.4	30	6	AR368286 Sequence
13	10	47.6	17	6	AX736243 Sequence
14	10	47.6	18	6	AX229718 Sequence
15	10	47.6	18	6	AX402871 Sequence
16	10	47.6	18	6	AX822220 Sequence
17	10	47.6	18	6	AX825860 Sequence
18	10	47.6	20	6	A32141 Synthetic C
19	10	47.6	20	6	A52459 Sequence 3

C 20	10	47.6	20	6	AR111715	AR111715 Sequence
C 21	10	47.6	20	6	CQ784255	CQ784255 Sequence
C 22	10	47.6	20	6	AR314772	AR314772 Sequence
C 23	10	47.6	20	6	AR315108	AR315108 Sequence
C 24	10	47.6	20	6	AR315109	AR315109 Sequence
C 25	10	47.6	20	6	AR337038	AR337038 Sequence
C 26	10	47.6	20	6	AX296790	AX296790 Sequence
C 27	10	47.6	20	6	AX537665	AX537665 Sequence
C 28	10	47.6	20	6	AX537695	AX537695 Sequence
C 29	10	47.6	20	6	AX956649	AX956649 Sequence
C 30	10	47.6	20	6	BD128179	BD128179 Primer fo
C 31	10	47.6	21	6	AR164118	AR164118 Sequence
C 32	10	47.6	22	6	A48928	A48928 Sequence 6
C 33	10	47.6	22	6	AR153363	AR153363 Sequence
C 34	10	47.6	22	6	AX801579	AX801579 Sequence
C 35	10	47.6	22	6	AX805811	AX805811 Sequence
C 36	10	47.6	23	6	AR237824	AR237824 Sequence
C 37	10	47.6	24	6	AR526704	AR526704 Sequence
C 38	10	47.6	24	6	AX292157	AX292157 Sequence
C 39	10	47.6	24	6	AX444019	AX444019 Sequence
C 40	10	47.6	24	6	AX445110	AX445110 Sequence
C 41	10	47.6	24	6	AX445735	AX445735 Sequence
C 42	10	47.6	24	6	AX445982	AX445982 Sequence
C 43	10	47.6	25	6	A45566	A45566 Sequence 4
C 44	10	47.6	25	6	A47604	A47604 Sequence 4
C 45	10	47.6	25	6	AR019330	AR019330 Sequence

ALIGNMENTS

RESULT 1	CQ824575	Sequence 2 from Patent WO2004047872.	21 bp	DNA	linear	PAT 21-JUN-2004
LOCUS	CQ824575					
DEFINITION	CQ824575					
ACCESSION	CQ824575					
VERSION	CQ824575.1	GI:49021594				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Kaemmerer, W.F.				
AUTHORS		Treatment of neurodegenerative disease through intracranial				
TITLE		delivery of sirna				
JOURNAL		Patent: WO 2004047872-A 2 10-JUN-2004;				
FEATURES		Medtronic, Inc. (US)				
source		Location/Qualifiers				
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Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	AATTCGTTGCTCGCTCTTGG	21	

RESULT 2

CQ824577	Sequence 4 from Patent WO2004047872.	21 bp	DNA	linear	PAT 21-JUN-2004
LOCUS	CQ824577				
DEFINITION	CQ824577				
ACCESSION	CQ824577.1	GI:49021598			
VERSION	CQ824577.1				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

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REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      1
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  AATCGTTGCTCCGCTCTTGG 21
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Db   1  AATCGTTGCTCCGCTCTTGG 21
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RESULT 3
CQ824574/c
LOCUS      CQ824574      21 bp      DNA      linear      PAT 21-JUN-2004
DEFINITION Sequence 1 from Patent WO2004047872.
ACCESSION  CQ824574
VERSION     CQ824574.1 GI:49021592
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Kaemmerer, W.F.
JOURNAL    Treatment of neurodegenerative disease through intracranial
           delivery of siRNA
           Patent: WO 2004047872-A 1 10-JUN-2004;
           Medtronic, Inc. (US)
FEATURES   source
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3  TTCGTTGCTCCGCTCTTGG 21
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Db   21 TTCGTTGCTCCGCTCTTGG 3
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RESULT 4
CQ824576/c
LOCUS      CQ824576      21 bp      DNA      linear      PAT 21-JUN-2004
DEFINITION Sequence 3 from Patent WO2004047872.
ACCESSION  CQ824576
VERSION     CQ824576.1 GI:49021596
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Kaemmerer, W.F.
JOURNAL    Treatment of neurodegenerative disease through intracranial
           delivery of siRNA
           Patent: WO 2004047872-A 3 10-JUN-2004;

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FEATURES     source
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QY  3  TTCGTTGCTCCGCTCTTGG 21
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Db   21 TTCGTTGCTCCGCTCTTGG 3
      |||||

RESULT 5
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LOCUS      AR568156      22 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 81 from patent US 6781028.
ACCESSION  AR568156
VERSION     AR568156.1 GI:53986443
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Costa, M.R.; Doberstein, S.K.; Elson, S.L.; Ferguson, K.C. and
           Homburger, S.A.
TITLE      Animal models and methods for analysis of lipid metabolism and
           screening of pharmaceutical and pesticidal agents that modulate
           lipid metabolism
           Patent: US 6781028-A 81 24-AUG-2004;
           Location/Qualifiers
FEATURES   source
              1. .22
              /organism="unknown"
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ORIGIN
Query Match      57.1%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  ATTCGTTGCTCC 13
      |||||
Db   11 ATTCGTTGCTCC 22
      |||||

RESULT 6
AX463675
LOCUS      AX463675      30 bp      DNA      linear      PAT 15-JUL-2002
DEFINITION Sequence 13 from Patent WO248185.
ACCESSION  AX463675
VERSION     AX463675.1 GI:21886434
KEYWORDS   Synthetic construct
SOURCE     Synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 Subtil, A., Parsot, C. and Dautry-Varsat, A.
AUTHORS    Secreted chlamydia polypeptides and method for identifying such
TITLE      polypeptides by their secretion by a type III secretion pathway of
           a gram-negative bacteria
           Patent: WO 0248185-A 13 20-JUN-2002;
           INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
           SCIENTIFIQUE (CNRS) (FR); INSERM (E.P.S.T.) (FR)
JOURNAL
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCGTGTGCTC 12
    |||||
Db 6 AATCGTGTGCTC 17

RESULT 7
E30575/c
LOCUS Neurogenesis-inductive gene. 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Neurogenesis-inductive gene.
ACCESSION E30575
VERSION E30575.1 GI:13017145
KEYWORDS JP 1999341985-A/28.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Katuhiko,M., Jun,A., Kenji,N. and Katsunori,N.
TITLE Neurogenesis-inductive Gene
JOURNAL Patent: JP 1999341985-A 28 14-DEC-1999;
COMMENT RIKAGAKU KENKYUSHO
OS Unidentified
PN JP 1999341985-A/28
PD 14-DEC-1999
PF 30-APR-1998 JP 1998121456
PR KATSUHIKO MIKOSHIBA, JUN ARIGA, KENJI NAGAI, KATSUNORI NAKATA PC
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K38/00, A61K48/00, PC
C07K14/47
PC C12N1/21, C12N5/10, C12P21/02/(C12N15/09, C12R1:91), (C12N1/21,
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PC (C12N5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:19),
PC C12N15/00,
PC A61K37/02, A61K37/02, C12N5/00, (C12N15/00, C12R1:91), (C12N5/00,
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CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGGCTCTTG 20
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Db 11 CTCGGCTCTTG 1

RESULT 8
AR268863/c
LOCUS Sequence 31 from patent US 6500637. 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 31 from patent US 6500637.
ACCESSION AR268863
VERSION AR268863.1 GI:29699559
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mikoshiba,K., Aruga,J., Nagai,T. and Nakata,K.

ORIGIN
Query Match      57.1%; Score 12; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCGTGTGCTC 12
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Db 6 AATCGTGTGCTC 17

TITLE Neurogenesis inducing genes
JOURNAL Patent: US 6500637-A 31 31-DEC-2002;
FEATURES
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Location/Qualifiers
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ORIGIN
Query Match      52.4%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTCGGCTCTTG 20
    |||||
Db 11 CTCGGCTCTTG 1

RESULT 9
AR442594
LOCUS Sequence 202 from patent US 6670130. 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 202 from patent US 6670130.
ACCESSION AR442594
VERSION AR442594.1 GI:42669851
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,C.M., Park,H.K. and Jang,H.J.
TITLE Oligonucleotide for detection and identification of Mycobacteria
JOURNAL Patent: US 6670130-A 202 30-DEC-2003;
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Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
Query Match      52.4%; Score 11; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTTGCTCCGCT 16
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Db 10 GTTGCTCCGCT 20

RESULT 10
AR098219/c
LOCUS Sequence 42 from patent US 6074851. 30 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 42 from patent US 6074851.
ACCESSION AR098219
VERSION AR098219.1 GI:12807476
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Deibel,W.R. Jr., Yem,A.W. and Wolfe,C.L.
TITLE Catalytic macro molecules having cdc25B like activity
JOURNAL Patent: US 6074851-A 42 13-JUN-2000;
FEATURES
source 1..30
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGCTCCGCTC 17
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Db 14 TTGCTCCGCTC 4

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RESULT 11
BD195066/c
LOCUS          BD195066          30 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Catalytic polymer having CDC25B like activity.
ACCESSION      BD195066
VERSION        BD195066.1 GI:33004824
KEYWORDS       JP 2002515742-A/27.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE       1 (bases 1 to 30)
AUTHORS        Jr,M.R.D., Yem,A.W. and Wilson,C.L.
TITLE          Catalytic polymer having CDC25B like activity
JOURNAL        Patent: JP 2002515742-A 27 28-MAY-2002;
COMMENT        PHARMACIA & UPJOHN CO
OS             Unidentified
PN             JP 2002515742-A/27
PD             28-MAY-2002
PF             02-MAY-1997 JP 1997538892
PR             02-MAY-1996 US 60/016748,07-MAY-1996 US 60/017323 PI
MARTIN R DEIBEL JR,ANTHONY W YEM,CINDY L WILSON PC
C12N15/55,C12N15/54,C12N15/62,C12N9/16,C12N9/10,C12N1/21// PC
(C12N1/21,C12R1:19)
CC             Strandedness: Single;
CC             Topology: Linear;
CC             Catalytic polymer having CDC25B like activity FH Key
CCT            Location/Qualifiers
FT            source          1. .30
FT            Location/Qualifiers
FT            /organism='Unidentified'.
FEATURES       source
source         1. .30
                /organism="unidentified"
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                /db_xref="taxon:32644"
ORIGIN
Query Match    52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TTGCTCGCTC 17
    |||||
Db 14 TTGCTCGCTC 4

RESULT 12
AR368286
LOCUS          AR368286          30 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION     Sequence 6 from patent US 6376240.
ACCESSION      AR368286
VERSION        AR368286.1 GI:34601963
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE       1 (bases 1 to 30)
AUTHORS        Song,A.M., Chen,Y.-F. and Krensky,A.M.
TITLE          RFLAT-1: a transcription factor that activates RANTES gene
JOURNAL        Patent: US 6376240-A 6 23-APR-2002;
FEATURES       Location/Qualifiers
source         1. .30
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match    52.4%; Score 11; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGTTGCT 11
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1 AATTCGTTGCT 11

RESULT 13
AX736243/c
LOCUS          AX736243          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION     Sequence 1833 from Patent WO03025177.
ACCESSION      AX736243
VERSION        AX736243.1 GI:30515520
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE       1
AUTHORS        Telerman,A., Anson,R. and Tuijnder,M.
TITLE          Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL        Patent: WO 03025177-A 1833 27-MAR-2003;
FEATURES       Molecular Engines Laboratories (FR)
                Location/Qualifiers
                source          1. .17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
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Query Match    47.6%; Score 10; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCGCTCTTGG 21
    |||||
Db 13 CCGCTCTTGG 4

RESULT 14
AX229718/c
LOCUS          AX229718          18 bp      DNA      linear      PAT 11-SEP-2001
DEFINITION     Sequence 5 from Patent WO0162933.
ACCESSION      AX229718
VERSION        AX229718.1 GI:15591930
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE       1
AUTHORS        Pantelidis,P.
TITLE          Muteins of interleukin-13 (11-13)
JOURNAL        Patent: WO 0162933-A 5 30-AUG-2001;
                Royal Brompton and Harefield NHS Trust (GB)
FEATURES       Location/Qualifiers
source         1. .18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PCR primer"
ORIGIN
Query Match    47.6%; Score 10; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTCCGCTCT 18
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Db 18 GCTCCGCTCT 9

RESULT 15
AX402871/c
LOCUS          AX402871          18 bp      DNA      linear      PAT 07-JUN-2002
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DEFINITION Sequence 355 from Patent WO0196612.
ACCESSION AX402871
VERSION AX402871.1 GI:21387862
KEYWORDS
SOURCE
ORGANISM Penicillium melinii
          Penicillium melinii
          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
          Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 355 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
    source
        1..18
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            /mol_type="unassigned DNA"
            /db_xref="taxon:69779"
ORIGIN
Query Match 47.6%; Score 10; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 TCCGCTCTTG 20
   |||||
Db 17 TCCGCTCTTG 8

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